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FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCAATGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAAGTCATTACTTGTTCAGAGCGTTCTGCTAATCTACACTTTTATTTTC
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA
CTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG
TCATTATTCCTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA
AACTGTATGCAATGTTTCTGACTCTCGTTTTTTGGTTCGAACTGGTCGCTGCCATCGTAGG
ATTTGTTTTGAGACATGAGATTAAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC
AGTATAACTCTACAGGAGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA
ATTTCCCTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTCTCGCCTACTGCCWCCTCTCG
TGCCATAACAAATAACCAAGTATGAGATAGTGTACCCAATGTATCTGTGGGCCATTCTCTCT
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAACCTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCATGTTAGATCG
TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

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FIGURE 2

```
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><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
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VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
```

Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTTCTCTCGGACCTGTACAAA
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCGGGAGGTAGAGAAAGTCAGT
 GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG
 GCCGGGGTAGGCTCTGGAAAGGGCCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCTTAGAAGAGGGT
 GTTCCCTCTTTCCGGGGTCTTACCAGAAGAGGTTCTTGGGGGTCGCCCTTCTGAGGAGGCT
 GCGGCTAACAGGGCCCCAGAAGTCCATTGGATGTCCAGAATCCCCGTAGTTGATAATGTTG
 GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTC
 TCAACTCCAGGTTATGAAAACAGTACTTGGAAAACGAAAACCTAAATGATCGTCTTTG
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG
 CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG
 CCGAGATGACAGTGGAAACAGATGACAGTGTGACACCCACAGCAACAGGCCGAGAACAGTG
 CAGTACCCACTGCTGACACAAGGAGCCAACCACGGGACCCTGTTTCGGCCACCAAGGAGGGC
 CGAGGACCTCATGAGCCAAGGAGAAAAGAAACAAAATGTGGATGGGCTAGTGTTGGACACACT
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT
 GAAAAGTGTTCTGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG
 CCAAGCCTTGCTGTCTACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA
 TGATAAGATTTGATGTTTTTGTCTGCTGTCTATCTACTTTGCTCTGGAATGTCTAAATGTTTC
 TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

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FIGURE 4

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDFVRPFRRGRGPHEFRRKKQNV DGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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FIGURE 5

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTCAGCCCATTGCGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCTAACGGACTG
CAAGCATGGAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT
CAGGTGCCTGGGGCATGCAAAATGTGGGTGACCTTCGTCTCAGGCTTCCTGCTTTTCCGAAGC
CTTCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCTTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGAGGTACCAGGCAGCCACCAGGGTCCCCTACCGCCAGCTGC
GAGAGAAGGACCCCAAGTACAGTGCTCTCCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC
TCTCTTTGCAATCTGGGCTGCGTCTTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA
AATAAGGAGCCTCTAGCATGGGCCCTGCATGCTAATAAATGCTTCTTCAGAAATGAAAAAA
AAAAAAAAAAAA

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FIGURE 6

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56107

<subunit 1 of 1, 231 aa, 1 stop

<NX(S/T): 0

MEEGGLGGLIKMVHLLVLSGAWGMQMVTFVSGFLLFRSLPRHTFGLVQSKLFPPFYFHISM
GCAFINLCILASQHAWAQLTFWEASQLYLLFLSLTLATVNARWLEPRTTAAMWALQTVEKER
GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCAGATTTTAAAGCCCATTTCTGCAGTGGAAATTTTCATGAACTAGCAAGAGGACACCATCTT
CTTGATTATTATACAAGAAAGGAGTGACCTATCACACACAGGGGAAAAATGCTCTTTTGGGT
GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACATAAGATTGAAG
ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAACTTGGCAGCC
AGAAGTTTTGATAAAAAGGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG
AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGGAGAAAGGTCTCTGGGGT
CTGATCAATAATGCTGGTGTCCCGGCGTGTGGCTCCCACTGACTGGCTGACACTAGAGGA
CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC
CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCCTTGCA
ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG
ACGGGACATGAAAGCTTTTGGTGTGCACGTCTCATGCATTGAACCAAGGATTGTTCAAAACAA
ACTTGGCAGATCCAGTAAAGGTAATTGAAAAAAAACTCGCCATTTGGGAGCAGCTGTCTCCA
GACATCAAAACAACAATATGGAGAAGGTTACATTGAAAAAAGTCTAGACAAACTGAAAGGCAA
TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
GTCTCTCCCTAAGACTCATTTATGCCGCTGGAAAAGATGCCAAAATTTCTGGATACCTCTG
TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
TCCAAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT
TTCAAGAACACATCTCCTTTTCAACCCCATTCCTATCTGCTCCAACCTGGACTCATTAGAA
TCGTGCTTATTTGGATTGCAAAAGGGAGTCCACCATCGCTGGTGGTATCCAGGGTCCCTG
CTCAAGTTTTCTTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCTGCCCTGT
ATTTAGGCTTTGCCCTGCTTGGTGTGATGTAAGGGAATTGAAAGACTTGCCCATTCAAAATG
ATCTTTACCGTGGCCTGCCCATGCTTATGGTCCCCAGCATTTACAGTAACTTGTAATGTT
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AAAAAAAAAAAAAAAAAAAAA

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FIGURE 8

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ESGSTALKAETSERLRVLLDVTDPENVKRTAQWVKNQVGEKGLWGLINNAGVPGVLAPTDW
LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVEKKLAIWEQLSPDIKQYGEQYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

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FIGURE 9

GCGGGCTGTTGACGGCGCTGCG**ATGG**CTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTGTAGCGCCGCAGTGGGCGGGGGCCCCTTGGGCGGTGCGCCACCCT
 TAGTCATGTACCACCCGCCCGCCGCCCGCTCATCGGGACTTCATCTCGGTGACGCTGAG
 CTTTGGCGAGAGCTATGACCAAGCAAGAGTTGGCGGGCGGCGCTGCTGCTGGAGGAAATGGA
 AGCAACTGTGCGAGATTGACAGCGGAATATGATTCTCTTCTCCTTGCCTTTCTGCTTTTCTGT
 GGACTCCTCTTCTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAATTGTGGGTTAAACCAGCAAAATCCACCCGCTCTTACCAG
 CTCTCAGAAGGCGGACACCGACCCTGAGAACTTACCTGAGATTTCGTCACAGAAGACACAA
 AGACACATCCAGCGGGGACCCTCACCTGCAGATTAGACCCCAAGCCAAGACCTGAAGGA
 TGGGACCCAGGAGGAGGCCACAAAAAGGCAAGAAGCCCCGTGGGATCCCCGCCGGAAGGAG
 ATCCGAGAGGACAGTCATCAGCTGGAGGGGAGCGGTGATCGAGCTGAGCAGGGCCACGAG
 CTCCCTTCAAGAAGAGCAGAAGTGCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
 CACACCACTGCATCTGAACTATCGCCAGAAGGGCGTGATTGACGCTTCTCTGCATGCATGGA
 AAGGATACCCGAAGTTTGCATGGGGCCATGACGAGCTGAAGCCTGTGTCCAGGCTCTGCTCAGT
 GAGTGGTTTGGCCCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT
 GAGGAAGAATTTGAGGAAGCCAGGAAGTGGGTGTGCAAGAAGTTACACTTTGAAAGGACG
 TGGACGTCAACCTGTTTGAAGACACGATCCGCATCCTGGGGGGGCTCCTGAGTGGCTACCAC
 CTGTGTGGGGGACAGCCTTCTCTGAGGAAAGCTGAGGATTTTGGAAATCGGCTTAATGCCTGC
 CTTTCAGAACACCATCCAAGATTCTCTACTCGGATGTGAACATCGGTACTGGAGTTGCCAC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCCGAGGTGACCAGCATCAGCTGGAGTTCGGG
 GAGCTCTCCGCTCTCACAGGGGATAAGAAGTTTCAGGAGCGAGTGAGAAAGTGACACAGCA
 CATCCACGGCCTGTCTGGGAAGAAGGATGGGCTGGTGCCCATGTTCAATACCCACAGTG
 GCCTCTTACCCACCTGGGCGTATTACAGCTGGGCGCCAGGGCCGACAGCTACTATGAGTAC
 CTGCTGAAGCAGTGGATCCAGGGCGGGAAGCAGGAGACACAGCTGCTGGAAGCTACGTGGA
 AGCCATCAGGGGTGTGAGAAGCACCCTGCTGCGGCACTCCGAGCCAGTAAGTCACTCTTTG
 TGGGGGAGCTTGCCACGGGCCGCTTCACTGCCAAGATGGACCACCTGGTGTGCTTCTGCCA
 GGGACGCTGGCTCTGGGCGTCTACCACGGCCTGCCCGCCAGGCACATGGAGCTGGCCCAGGA
 GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGGAGACGGGGCTGAGTCCCAGATCG
 TGCACTTCAACCTTTACCCCCAGCCGGGCGCTCGGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTCGGGCCAGAGACCTGGAGAGCCTGTTCTACCTGTACCGCGCTCACAGGGGA
 CCGCAAAATACAGGACTGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACAGGGTCC
 CCTCGGGTGGCTATTCTTCCATCAACAATGTCCAGGATCTCAGAAGCCCCGAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGGAGACGCTCAAGTATCTGTTCTTGCTCTTCTCCGATGA
 CCGAAACCTGCTCAGCTTGGACGCCCTACGTGTTCAACACCGAAGCCACCTCTGCTATCT
 GGACCCCTGCC**TAGGG**TGGATGGCTGCTGGTGTGGGACTTCGGGTGGGCAGAGGCACCTTG
 CTGGGTCTGTGGCATTTTCCAAGGGCCACGTAGCACCCGGCAACCGCCAAGTGGCCAGGCT
 CTGAACCTGGCTCTGGGCTCCTCTCGTCTCTGTTAATCAGGACACCGTGAGGACAAGTGA
 GGCGCTCAGTCTTGGTGTGATGCGGGGTGGGCTGGGCGCTGGAGCCTCCGCGCTGCTTCTC
 CAGAAGACACGAATCATGACTCACGATTGCTGAAGCCTGAGCAGGTCTCTGTGGCCGACCA
 GAGGGGGGCTTCGAGGTGGTCCCTGGTACTGGGGTGACCGAGTGGACAGCCAGGGTGCAGC
 TCTGCCCGGGCTCGTGAAGCCTCAGATGTCCCCAATCCAAGGGTCTGGAGGGGCTGCCGTGA
 CTCCAGAGGCTGAGGCTCCAGGCTGGCTCTGCTGTTTACAAGCTGGACTCAGGATCCCTC
 CTGGCCGCCCGCAGGGGGCTTGGAGGGCTGGACGGCAAGTCCGCTTAGCTCACGGGCCCC
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FIGURE 10

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IAGLKPANPPVLPAQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTPELPSRRAEVPTKPPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDEVNIGTGVAHPPRWTSDSTVAEVTSIQLEFREL SRLTGDKKFQEA VEKVTHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQETQLEDYVEAIEGVRT
HLLRHSEPSKLTFFVGELAHGRFSKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTEAHPLPIWTPA
```

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

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FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC
CGCCTCTCCGCACG**ATG**TTCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC
AGGTCCGGGTTGCTCTCGCGGGCCTCCCTCGGAAGTGTTCCGCTTCCACCTGTTCTGTGGC
CTGCCTCTCGTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGGACGTGG
CCCCGGCAGTCAAGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCCTGCCCCCAGAG
CCGCCCCCTGAGACTGGGAAGAAGACGCATCCTGGGGCCCCACCAGCTGGCAGTGTGTT
GCCCTTCCGCGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCACATGCGCCGCTTCTGA
GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAGGTGGACCACCTCAGGTTCAAC
CGGGCAGCGCTCATCAACGTGGGCTTCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT
GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC
CCTTCCACGTGGCTCCCGGAGCTCCACCCTCTCTACCACTACAAGACCTATGTGCGCGGC
ATCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG
CTGGGGCCGCGAGGACGACGAGTTCTACCGGCGCATTAAAGGAGCTGGGCTCCAGCTTTTCC
GCCCCCTCGGGAATCACAACGTGGGTACAAGACATTTGCCACCTGCATGACCCAGCCTGGCGG
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AGGCCTGAACACTGTGAAGTACCATGTGGCTTCCCGCACTGCCCTGTCTGTGGGCGGGGCC
CCTGCACTGTCTCAACATCATGTTGGACTGTGACAAGACCGCCACACCTGGTGCACATTC
AG**CTGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATATTGCTCAGGCTCAGGA
CAAGGCCTCAGGTCTGTGGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
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FIGURE 12

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RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPFAGPFHVA
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRRKRDQKRIAAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

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FIGURE 13

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCTATGCTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT
CTTCTGCCACTGACGCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGGAAGGGGAGAAAGT
GGGGGATGGCTAAGAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGGG
GCTGCCTTATTTAAAGTGGTTGTTTATGATTCTTATACTAATTTATACAAAGATATTAAGGC
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FIGURE 14

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56862

<subunit 1 of 1, 73 aa, 1 stop

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PRGEGEKVGDG**Important features:****Signal peptide:**

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCGGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAA
 GAGCATGTCGCGCGCGGGAGAGGCCCGCTCCTCCGGCCGCCATAAGGCTCCGGTCGCGCGTGG
 GCCCGCGCGGCTCCTGCGCCCGGGCTCCGGGGCGGCCCGCTAGGCCAGTGCAGCGCCG
 CTGCCCCGCGAGGCCCGGCCCCGAGC**ATGG**AGCCACCCGGACGCCGGCGGGCGCGCGCA
 GCCGCCGCTGTTGCTCGCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCGCGCGG
 CGCGCGGCGCGCGCGGCTGCCCGCGGCTGCAAGCACAGTGGCGGCGCCCGAGGGCTGGC
 AGGGCGGCGGCGCGCGGAGGGCAAGGTGGTGTGCAGCAGCCTGGAACCTCGCGCAGGTCTCT
 GCCCCAGATACTCTGCCCAACCGCACGGTCACCCCTGATCTCGAGTAACAATAGATATCCG
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 CTTATTAGTAGTATAGATCCAGGTGCCTTCTGGGACTGTCTATCTCTAAAGATTGGATCT
 GACAAACAATCGCAATAGGATGTCTGAATGCAGACATATTTCCAGGACTCAACATCTGGTTC
 GGCTAAACCTTTGCGGGAATTTGTTTTCTTCATTATCTCAAGGAACCTTTGATTATCTTGGC
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 CACTGCAGGCCCAACAGTCACAGGCGTGAAGCAGGAGCTGTTGACATGCGACCTCCGCTT
 GAATTGCGCTTTTCTACACTCCATCTCATCGCAAAGTTGTGTTTGAAGGAGACAGCTT
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 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAGAGCTAGGTGACGTGATGGTT
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 ACTTTCGGATTATGGGAGGCGGGATCCAGAGGGAAACCTGGAAGCTAGGTGACGTGATTAAGT
 GCAATGTTCAAAATACATTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT
 AAGACTATTTACAGT**TAA**ATTGAAGTCTCCAATGTTCTGCTTCGCAAAAATACCTTATTA
 AAAGATTTTTTTTTCAGGAAGATAGGTATTATTGCTTTTGCTACTGTTTTAAAGAAAAC
 ACCAGGAAGACTGCATTACGACTTTCAAGGGCCCTAGGCATTTTGCCCTTGATTCCCTTT
 CTTACATAAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTAAAGTGCATAATACT
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 TTGAAGCAAGCAAAATGAAAGACTTTTTACTGATTTTTTAAAGTTGGTCTTAGATATATTT
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 TACTTTATTTCTGTCTGTGCCCTCAATAATATCAGAAAACATATTCAGCTCATTTTAAATGGC
 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTCTGGTTTGTAGTGTGAGGACTCAATAAATA
 TTGAATGAATTGACGAAAAAAGAAAAA

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FIGURE 16

MEPPGRRRRGRAQPPILLPLSLLALLLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPPDTLPNRTVTLILSNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA
 FWGLSSLKRDLTNNRIGCLNADIFRGLTNLVRNLNLSGNLFSSLSQGTFDYLAASRSLEFQT
 EYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELLTCDPPELPSFYMTF
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT
 ISNIQAGSTGNWGCCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGFDRWPRTLAGITA
 YLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPNLN
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDMVDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNVSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,
 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,
 384-390, 403-409, 554-560

CGCTGGGGATGCTTAGAGAGCTCGAAGGTGGTGCTGGGCCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCCAAATTCGGA AAAAGAAAACATTCTGCTTTTGGGAGAACAGATTA
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAAGGATCTCAAAA
TCATTGACTTGAATGTGAAATATCTGTGGACAGACAACACGAGTTTGTGTGTGTGTTGAT
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTGGTCACTGTCCTTTAAACTTGATCA
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGCACTTTTGGAAAGTAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCAGTCTCCAGCTCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA
TGGATAGTAGCATCCACCTGAGTAGTCTGATGACTCGGCATGATGACGAAGCCACGAGAACA
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGGAGAGAGCTCCGTAGTCGTGCAATC

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FIGURE 18

MSRSSKVVGLSVLLTAATVAGVHVKKQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

FIGURE 19

CTGTCGTCTTTGCTTCAGCCGAGTCGCCACTGGCTGCCGTAGAGTGCTCTTACAGCCTGTTC
 CAAGTGTGGCTTAATCCGTCTCCACCACCAGATCTTTCTCCGTGGATTCCCTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGACCACCATCACACCACCACGACGTATCTTCGGG
 CCTGGGGTCCCCATGATCGTGGGGTCCCCGCGGCCCTGACACAGCCCCTGGGTCTCCTTCGC
 CTGTGTCAGCTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGTAGCGTGGGCGCCTGGAC
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTCTGCTTCTCCGTGACCCTGATCA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCCGCTTCCCCCTGTCTTGGCGCAACTTCCCC
 ATCACCTTCGCCTGCTATGCGGCCCTTCTTGCCTCTCGGCCCTCCATCATCTACCCACCAC
 CTATGTCCAGTTCCCTGTCCCACGGCCGTTCCGCGGACCACGCCATCGCCGCCACCTTCTTCT
 CCTGCATCGCGTGTGTGGCTTACGCCACCAGAGTGGCCTGGACCCGGGCCCGGCCGGCGAG
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGTGCTGGAGACCTTCGTTGCCTG
 CATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACCAGCACCGCGGCCCTGGAGTGGT
 GCGTGGCGGTGTACGCCATCTGCTTCATCTAGCGGCCATCGCCATCCTGTGAACCTGGGGG
 GAGTGCACCAACGTGTACCCATCCCCCTTCCCCAGCTTCTGTGCGGGCTGGCCTTGTCTGT
 TGTCTCTCTATAGCCACCGCCCTTGTCTCTGGCCCCCTTACCAGTTCGATGAGAAGTATG
 GCGGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT
 GCCTGGGACCGCCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACCTCTGCCACCTGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC
 CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCCGAGTTTTCTTTATGGAGTACTTCTTTCC
 TCCGCCCTTCTCTGTTTTCTCTTCTCTCCCTCCCTCCACCTTTTTCTTTCTCTTCC
 CAATTCCTTGCACTCTAACCAGTTCTTGGATGCATCTTCTTCTTCCCTTCTCTTCTGT
 TTCTTCTCTGTGTTGTTTGTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT
 CTTTCTTCTCTTTTTTTTTTTTTTTTTTAAAGCGGATTCTCACTCTGTGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTCACTGCAACCCCGCCTCCTGGGTTCAAGCGATTCTCTCC
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTTCTCTTT
 TTCCACTCTTCTTTTTTCTCATCTCTTTTCTGGGTTGCCTGTCGGCTTCTTATCTGCCTGT
 TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTTCTCTCTTGCCTCCA
 CCCACCTCCAAGGTGCTGAGCTCACATCCACACCCCTTGACGCCGTCCATGCCACAGCCCC
 CCAAGGGGCCCCATTGCCAAAGCATGCCGTGCCACCCCTCGCTGTGCCTTAGTCAGTGTGTAC
 GTGTGTGTGTGTGTGTTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGCCCTCTTCT
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCTTTAAATTAAAAAACATATATATATATAT
 ATTTGGAGGTCAGTAATTTCCAATGGGCGGGAGGCATTAAGCACCGACCTGGGTCCCTAGG
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC
 CCACCTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCAACTATTCT
 CTGTGGTATGAAAAAG

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FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTRTTITTTTTSSSGLGSPMIVGSPRALTQPLGLLRLLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLIILIVELCGLQARFPLSWRNFPIITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIIACVAYATEVAWTRARPEITGYMATVPGLLKVLETFFVACI
IFAFISDPNLYQHQPALWCVAVYAIICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

[illegible]

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FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSLAQVNLSPFSPKVMHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPLSPGISQVVKDHVTKPTAMAGQGRVAHLIEWKGWSKPSDSPAALSAFSSY
SDLSEGEQEARFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLDGGLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

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FIGURE 23

GGTTCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAATTTGTTTCCCT
 GGCACCTCCTGCTCAGTGCGACATTGTCACACTTAACCCATCTGTTTTCTCTAATGCACGA
 CAGATTCCTTTAGACAGGACAACCTGTGATATTTAGTTCTCTGATTGTAAATACCTCCTAAG
 CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA
 TACAATCTATTCTTCCACATCAAGGGATTGTTATTCCTTTAAAAAAAACCAATACCAAAG
 AAGCCTACAAATGTGGCCTTAGCCAAAATTCTGTTGATTTCACGTTGTGTTTTATTCACTTCT
 ATCGGGGAGCCATGGAAGAAATAAAGACATAAACACAAACACAGAACATTGCAGAAGTTT
 TTAAACATGGAATAAACTATTCTTTGGAAGTGAAGCAAACCTTAACTCAGATAAA
 GAAATATAACCACTCAAATCTCAAGGCGAGTCATTCCCTCCTTTGAATCTACCCAACAA
 CAGCCACGGAATAACAGATTTCTCCAGTAACTCATCAGCAGAGCATTCTTTGGGCAGTCTAA
 AACCACATCTACCATTCCACAAGCCCTCCCTTGATCCATAGCTTTGTTCTAAAGTGCCCT
 TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC
 TGCTCTGTCTTCAGAAACTTCACTTGGTCTTTGGTCAATGACACCGTGAAGAACTCCTGATA
 ACAGTTCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCTTG
 ATAGTGGAAACCAAGTGATGGCTTACCACAACAGTGATAGCTTCACTGGGTTTACCCCTTA
 TCAAGAAAAACAACCTACAGCCTACCTTAAAAATTCACCAATAATTCAAAACTCTTTCCAA
 ATACGTGAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTCGGGGCCATTTTAGGT
 GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTGTGTGGAAGAAAGGAAAC
 GGATTCATTTTCCCATCGGCGACTTTATGACGACAGAAATGAACCAGTTCTGCGATTAGACA
 ATGCACCGGAACCTTATGATGTGAGTTTTGGGAATTCTAGCTACTACAATCCAACCTTGAAT
 GATTACGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
 TCCACTTCGTACTTCTGTATTAGAACTAACAGCAAAAGGCGTTAAACAGCAAGTGTCATCTA
 CATCCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTAAGTGCACGTGGAT
 TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAATGTAGACAGGATGTATCAT
 CCAAGGTTTTCTTCTTACAATTTTGCCCATCCTGAGGCATTTACTAAGTAGCCTTAATT
 TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAACTAAAGATT
 TCACCATACAGCCCTGCCTATAACTAAATAATAAAATTTATCCACCAAAAAATTTCTAAA
 ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCAATAATTCAAGATTGCAT
 TTTCTTAAATGAAAATTGAAAGGGTGCTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG
 GACATAGCCAGAGTTTCTGTTATTGGGAATTGAGGCAATAGAAATGACAGACCTGTATTC
 TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA
 CAATGACTGCATTCAACGGGGCCATGGCAGGAAGCTGACCTACCCAGGAAAGTAATAGCT
 TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTTAACTTGCTTAAATATATCTTAGGCTTCAA
 TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732

><subunit 1 of 1, 334 aa, 1 stop

><MW: 36294, pI: 4.98, NX(S/T): 13

MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSEFVSKVPWNA
PIADEDLLPISAHPNATPALSSSEFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTNDSDFTGFTPYQEKTTLQPTLKFNNKSLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTDSEFSHRLYDDRNEPVLRLDNAPEPYDVSEFGNSSYYNPNTLNSA
MPSESEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC
 AGCCCGAAGATTCACTATGGTGAAAATCGCCTTCAATACCCCTACCGCCGTGCAAAAGGAGG
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCCTTTCATTTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT
 TCATGCCCAGAGCACCATTACCCTGGAGAGATGTGCTTTTTTGATTCTGAGGATCTGCA
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGACATTCGTGA
 GGATGACAAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCCCTGAG
 CAATTATTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTTGCTGGGGAAGTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA
 AAGTCTTCCGCCTTCGTGCGAGAGACCTCTGCTGGGTTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGATCTGCAAGAGT
AAGAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA
 CATTAAGGTTTATGGGATACTCAAGATATTTACTCATGCATTTACTCTATTGCTTATGCTTT
 AAAAAAGGAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAT
 TGGCATTGCTTGTTTTTTGAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATCCATCC
 GTTGTTTTTTTGTTGTTGTTTTTCTTTTCCTTTAAGTAAGCTCTTTATTCATCTTATG
 GTGGAGCAATTTTAAATTTGAAATATTTTAAATGTTTTTGAACTTTTTGTGTAAATATA
 TCAGATCTCAACATTGTTGGTTTCTTTTGTTCATTTTGTAACCTTCTTGAATTTAGA
 AATTACATCTTTGCAGTCTCTGTTAGGTGCTCTGTAATTAACCTGACTTATATGTGAACAATT
 TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCTACAA
 CCCTATAATAAATTTTACTCTATACAAAAA

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FIGURE 26

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCMLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSPAIIHDFEKGMTAYLDDLLGNCYLPLNTSIVMPCKNLVELFGKLAGS
RYLPQTYVVREDLVAVEEIRDVSNLGIFIYQLCNNRKSFRLLRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

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FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCCAGCCAGAGCAGCCCCGGGCACACGACTCTCT
CTTCCAGCCAGGTGCCCCCCACTCTCGCTCCATTGCGCGGGAGCACCCAGTCTGTACGCC
AAGGAAC TGGTCTGGGGGCACCAATGTTTTGCGCGGCAGCCCCAGCCTCCTCATCCTTCTG
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCCTCTGTGCCCTGAAGGCCACGTT
CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCTCCTCCCCGAGCTCC
CGCCACCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCACAACCTGGGG
GGCCCATACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCGCCAGTACGTGAT
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTCTGCTGATGTTTCATCGTCTGTGCCCGGTCAT
TCACCCGGCAGAAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTTCCCCAAGAAGAAGTAC
GTGGACAGAGTGACCGGGCGGGGGCCCCCGGCCTTCAGTGAGGTCCCCGACAGAGCCCC
CGACAGCAGGCCCGAGGAAGCCCTGGATTCTTCCCGCAGCTCCAGGCCGACATCTTGGCCG
CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG
GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGGACCAAGGAAGTCCA
GGGACATGGGGTCCAGTGGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCTTG
AGGGGGCTGTGTTGGCCGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTTTGTTAGCCAG
GAAGCCAGGGACCACTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCACCCAG
TGCTTAACAGTCTTCCCGGCTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTCACCTCCCC
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCTCCTGTGG
TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGA
GGAATCTTACCAAGTGCCATCATCCTTACCTCAGCAGCCCCAAGGGCTACATCTACAGC
ACAGCTCCCCTGACAAAGTGAGGGAGGGCACGTGTCCCTGTGACAGCCAGGATAAAACATCC
CCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAAC TACTTTTTAAACA
GCTACAGGGTAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTTCTGAAGG
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTTAAATCCTC
TCAAGCGCTCTCCAAGCACCCCGGCTGGGGGTGAGTTTCTCATCCCGCTACTGTGCTGG
GATCAGGTTGAATGAATGGAACCTTCTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG
GCTGTGTTTGAAGGGACCTCCACCTGGGGAAGTCCGAGGGGTGGGAAGGGTTTCTGACG
CCCAGCTGGAGCAGGGGGGCCCTGGCCACCCCTGTGCTCACACATTGTCTGGCAGCCTG
TGTCACCAATATTCTGCTAGTCTCGACAGGGAGCTGGGCTCCGTCTGCTTTAGGGAGGCT
CTGGCAGGAGGTCTCTCCCCATCCCTCCATCTGGGGTCCCCCAACCTCTGCACAGCTCT
CCAGGTGCTGAGATATAATGCACCAGCACAAATAAACCTTTATTCGGCCTGAAAAAAAAA
AAGA

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FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLILLLLLLLGSPATDARSVPLKATFLEDVAGSGEAE GSSASSPSLPPPWPAL
SPTSMGPQPTTLGGFSPPTNFDGIVDFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAAALGGGDGARMVEGRGAEEEEEGKSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

[illegible]

FIGURE 31

GACCGGTCCTCCGGTCTGGATGTGCGGACTCTGCTGCAGCGAGGGCTGCAGGCGCCGCGGGCGGTGCTCACCG
 TCGCCTGGCTGGTGGAGTTTCTCTCTCTTGTGCTGACCATGTTGTTCCTTGTGCTGGAATATTACCGGGACATCTTCA
 CTCTCTGCTGCGCTGCACCGGAGCTTGGTGTGTGCGAGGAGAGTGAGGGGAAGATGTGTTTCTTGAACAAGC
 TGCTGCTACTTGTGTCCTGGGCTGGCTTTTCCAGATTCCCACAGTCCCTGAGGAGCTGTGTTCTTGTGGAGAGG
 GTCCCTCATATGCTTTGAGGTGGACACAGTAGCCCCAGAGCATGGCTTGGACATGCGCCTGTGGTGGACCCAGC
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAAACTGCTCGCTTCTGTGGGTGTACGGCAGTAGTG
 CACGGAGTGGGGCTTCATGAGGAAAATCACCCCCACCACTACCACAGCTGGGAGGCCAGCCTTCCAGAGCCA
 CGCAGGGGCTGCAGGCACAGCTCGCCACAGGCCCTTTTCCACAACAGCGCCGCTCTTGCGCCGAGCCGTAGAGT
 TCGTGGCAGAAAGAAATTGGATCAAACTGTGTCAAACATATCAAGGCTACACTGGTGGCAGATCTGTTGCCCCAGG
 CAGAGTCACTTCTCAAAGAGCAGCTGGTGACACAGGAGAGGAAGGGGAGACCACAGCCAGCTGTTGGAGATCT
 TGTGTTCCCGAGCTGTGCCCTCACGGGGCCCAGGCATTGGCCCTGGGGCGGAGTTCGTGCAAGGAAGAGCCCTG
 GGGCTGTGCGGGCGCTGCTTCCAGAGGAGACCCCGGAGCCGTTCTGAGCAGTGCAGAGAACTTGTGTGGGGC
 TTGCAACAGAGAAAGCGTGTGCTTGGCTGTGACGCAACATCACAGCACTCATGAGGAGGGAGGTGAAGACAGCAG
 TGAGTCGCACACTTCGAGCCAGGGTCTGAACTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGCGCTGAC
 TGCTCTCTCTTGGCCGTGGGGCCACGGGACCTGACGAGGGAGTCTCCCCACAGCATCTGGAACAGCTCCTAGGC
 CAGCTGGGCCAGAGCGTGGCGGTGCCCGCAGTTCTGTGCCACCTGCTGAGCAGCATCTGGCAAGTCTCTGTG
 GAGTTAGCTTCCCTCCTCGTTGCAGATCAAACTCCTATCCTAGGGCCCCGGCACAGTACAGGCTGGAGAGAGG
 CAGGCTCGAAGGCTTCTGCACATGCTGCTTTCCTTGTGAAGGAAGACTTTCAGGGGCGCGTCCGCTGCAGCTG
 CTGCTGAGCCCAAGAAATGTGGGGCTTGTGCAGACACAAGGCCAAGGGAGTGGAGTCTGTGCTATTCTTCTA
 CGGGAGCTGGTGGAGAAGGCTGTGATGGGACGATGGAGATAGAGGCTGCTTGGGACGCTCCACAGGCCAG
 TGGCCAGGGACTTTGCTGAAGAATTTGACAACTGTCTAATCTGTTCTAGCCGAGGCCCACTGCCAGAACC
 CAGCTAAGAGCCTGTGAGTTGGTGCAGCCAAACCGGGGCACTGTGCTGGCCAGAGCTAGGGCTGAGAAGTGGCC
 CTGCTTGGGCAATTGCACAGAACCTGGACCCCCCCTCACGAGGAGGCCAAGTGCCCAATGCAGACCTCAG
 TGGTGGGGGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGCTGTCACTGGCTGGCATCCACACAGCGA
 ATCTTAGAGGAAGGAGAGTTGGCCGTATTGGGATTATGGCAGAAAAGTCCAGAGATCGAGCTCTGGATAGAA
 GAGGTGGTGTGTTTATCTCTTGGATACTAAATGAATCAGGTGTGTGGGCTGTCAACACAGAATTCAGGCT
 CATTTGCTATACCCGCTCTGTGAGAACTTTGAGCTTTGGAATTCAGACAGGCAAACTACTCGTCTTAAC
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTTCTATACAGGAGCTTGGAGTCCCATCTCTT
 ATAAATGCTTAACACAGGCGGGCTGTGGGCTCATGCTGTAATCCAGCTACTCAGAGGATGAGGAGGACCTGCTTGAAC
 GACTCGCTGAGGTGAGGAATCAAGACCAGCTTGGCCAACTATGGCAAAACCCCATCTACTATAAAATAAAAAA
 TTATTAGTGGGCCATGGTGGTGTGTGCCCTGTAATCCAGCTACTCAGAGGATGAGGAGGACCTGCTTGAAC
 CTGGAGGTGGAGGTTCAGTGAAGCCAGGTGCGACCACTGCACCTCAAGTGTGGTAAACAGAGAGAGACTTTCTAG
 AAAAAAGCTAAACAAACAGATAAGGTAGGACTCAACCAACTGAAACCTGACTTTCCCTGTACCTTCAGCCCTG
 TGCAGGTAGTAACCTCTGAGACCTCTCCCTGACAGGGACCAAGCACAGGCAATTTAGAGCTTTTATAGATAAA
 CTCGGTTTCTTTAAAAAAAAGGGCGGCGCCCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT
 TTTTCTTTTCTTTTCTTTTAAAAAGGGCTTTTATTTAAATCTCTCCCAACAGATGGCTCTTGCATCTGCCACAGCTC
 TGGGCGCTGCTGTGAGGAAAAGGCTGTTTCTTGGGCTGAGGCGGGCTGGGCTGTGCTAGGTCTGGCGGAGCTG
 CGCGTGTCTGGCGCCTTGGCTGTGCTAGCTGCTTCTTCCCGGACAGAGCTGCGGGTGTCTGAGTGTGCTG
 AGCTAAGAGAGCTCTGTGTCAGGGGTGGAGGCTGTCTTAAACGACACCTTGAGTGTCTGAGTGTGCTGAGTGTG
 GGTCCACCTGAGTGGCACGGGAGCAGCTGTGGCGGTGCTCTCTYTAGGCCAGTCTCTGGGAAACTAAGCT
 GGGCCTCTTTCTTAAAGACCGAGGATGGGTGGGTGGGTGGGAGTCACTGGGAAATGGCTGAGGAGCTACGTGT
 GAAGAGGGCGCGGTTTGTGGCTCAGCGGCTGTGAGCGCTCTCTCTGAGGCTCAGTTTCCCTTCCGTTCTA
 ATGAAGAACATGCGGCTCTGGTGTGTCTCAGGCTATTAGGACTTGGCTGAGGAGTGGGCTTGGAGCGGCTGAT
 GTTATTTTCAAACTGCTCTGCGAGCTTGGCTTGGCACGTATGGAATGGGCCATGTCCCTCTGCTGCGTGGAC
 GTCCGGTGGGAGTGGCGAGCCAGAGGCGGGGCGAGCTGCGCTGGGGGTGAGGGAGGCGCCCGGAGGG
 CCTCACAGAAAGTTGGCTCCGCAACACAGGACAGGCGGGCTCCGCGCGCGCCGCGCCAGCCCTCAGG
 GGCCGGTAGACAAGTGAAGTCCGCTGTGGCTGCTGCGCAGCAGGTAGCCCTGTATGTCAGTGGCGAGCGG
 TCGTCCGCGAGCTGGAAGCAGCGCCGCTCCACGACGAAACCGGCTGCGCT

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FIGURE 32

MCFLNKLLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPPEHGLDNAPVVDQQLLYTC
CPYIGELRKILLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP
SLRRTFVEFVAERIGSNCKVHKIKATLVADLVRQAESLLQEQLVTQGEEGGDPQLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAGVLATEKACAWLSANITAL
IRREVKAASRTLRAGQPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGCTCTGGTGGCTGGTTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAACTG
 AAGACTCTCTGCTTTTGGCCACAGCAGTTCCTGACGCTTCCTTGAGGTGTGAACCCACATCCC
 TGGCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG
 AGTAGCAACAAAGAGCAGCGGTCAGCAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTGCCAATGAGGTCCTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCAACCTCAAGAGTGGAGCATCACTGACGGCTATGTCCCCATTCTCGGG
 AACAAAGACTGCCCTCTCGGTGCCACCAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCCTCGTGGCCCATCC
 AGTGTGTTCCGCGTGTCTGAGGAGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT
 CATCTTCTGGGGGCCCGGAGCAAGATGCAAGAAGCCCGAGGGCAGCCTCGTGGTGTGATCC
 AGCGAGCGGGCCTGGTGTTCGCCAACATGGAAGCATATGCCGTCTCTCCCGGCCGATGCCG
 CAATTTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT
 GAGCACAGGCTGGTTTACCATGGTGATCGCGGTGGAGTTGTGTACACAGTGCATGTCTATG
 GCATGGTCCCCCACTACTGCAGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC
 TACGAGCCCAAGGGGCCGAGCAATGTGTCACTTACATCCAGATGAGCACAGTCCGAAGGG
 CAACCACCACCGCTTCATCACCAGAAAAAGGGTCTTCTCATCGTGGGGCCAGCTGTATGGCA
 TCACCTTCTCCACCCCTCTCGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCTCCAGCCAATCAGGGCC
 TGGGGAATCTGTTGGCAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCTTTCCCATGAGGCCTTGTTTCAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCAAGGAGCTGGGAATCTGGTGTG
 CCCCCTCAATTTCCAGCACCAGAAAGAGAGATTGTGTGGGGGTAGAAGCTGTCTGGAGGCC
 GGCAGAGAATTTGTGGGGTGTGGAGGTTGTGGGGGCGGTGGGAGGTCCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTGGGCTCTGCCCTGAGACCTTGACAAACCCCTCCCCCTCTCTGGG
 CACCTTCTGCCACACCACTTTCCAGTGCAGGAGTCTGAGACCCCTTTCCACCTCCCCATA
 GTGCCCTCGGGTCTGTCTCCCGTCTGGACCCCTCCAGCCACTTCCCTTGCTGGAAGGT
 CAGCTCTTTGGGGGTCTGGGGTGACCTCCCCACCTCTCGGAAACCTTTAGGGTATTTTTGC
 GCAAACCTCTCAGGGTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT
 TAGCCCTCAGGCAGCTGCCATTAGCTTTGGCTCTTAAAGGGCCAGGCCTCCTTTTCTGGCCT
 CTAGCAGGGAGGTTTTTCCAACCTGTTGGAGGCGCCTTTGGGGCTGGCCCTTTGTCTGGAGTCA
 CTGGGGGCTTCGAGGGTCTCCCTCGACCTCTGTCTGCTGGGATGGCTGTCTGGGAGCTGT
 ATCACTGGGTCTGTCCCTGGCTCTGTATCAGGCACCTTTATTAAGCTGGGCCCTCAGTGG
 GGTGTGTTGTCTCTGCTCTTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACAGATGGAGGAGGCCAGCAGCTAGCATTGCACACTGGGGTGATGGGTGG
 GGGCGGTGACTGCCCCAGACTTGTTTTGTAATGATTGTACAGGAATAAACACACCTACGC
 TCCGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 34

MSSNKEQRSVAVFVILFALITILILYSSNSANEVPHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCIVIVSSSSHLLGTKLGPEIERAECTIRMNDAPTGYSAADVGNKTTYRVVAH
SSVFRVLRPPQEEFVNRTFPETVFIFWGPPSKMQKPQGS�VRVIQAGLVPFNMEAYAVSPGRM
RQFDDLFRGETGKDKREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPIH
YYEPKGPDECVTYIQNEHSRKGNNHRRFITEKRVFSSWAQLYGITFSHPST

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

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FIGURE 35

GTTCTCATAGTTGGCGTCTTCTAAAGGAAAACTAAAATGAGGAACAGCGGACCGGGAGCAGCGAGCTT
 GAGGGAAGCATCCCTAGCTTTGTGGCGAGAGGGGCGAGGCTGAAGCCGAGTGCCCGAGGTTGTCTGAGGGCGTGG
 GGCAAAAGGTGAAGAGGTTTCAGAACCAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGCAGATTATACCGT
 CTGAGGTTAGCAGCTCCGAACATAGAGAAGTGGAGTGTGCGCAGGGAGCGAGCATATCTCTTTGTGTGACCTGGC
 GCCTATGGGACCTTGGCTTCAGACTTTGTGATACACCACTGCTGGGACGATGACGGCGTGGAGAGGAATG
 AGGCGTTCAGGTCACACTGGCTTCTCTCTTACGACAGCAGTGTGCTTGTGCTACTTTGACAGAGTCCCTCAG
 GTCACTGTCAGGCTGGCTCCAGCTCCAGAGCCCGGAGGACACTGTGATCTGGGCTGGGTGGGAAGTCCCA
 AGGATGAATGTAACTGGCGCTTGAATGGAAAGGAGCTGAATGGCTGGATGATGCTCTGGGTGTCTCTATCAC
 CACGGGACCTCTGTCATCACTGCCCTTAAACAACCACTGTGGGACGGTACCAGTGTGTGGCCGGATGCTCTGG
 GGGGCTGTGGCCAGCGTGGCAGCCTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGACCGTG
 ATTGAAGTGGATGAGGGAACACAGCAGCTATGCTTGCCTGCCACCTGCCGTGAGAGCCACCCAAAGCCAGGTCCGG
 TACAGGCTCAAAACAGAGTGGCTGGAGGCTCCAGAGGTAACCTGATCTGACCTTACGCTCAGGAGGATCCAGATT
 GTGAATGCCAGCAGGAGGAGGAGGAGGATGTACAAGTGTGCAAGCTACAACCAAGTACCAGGAAGTGAAGAAC
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGTGGAGCTGCCCGCATCTCTACCCCCAGAGGCC
 CAAACCTCATCTGTCACCAAGGCGCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAAATCCCCACCCCGAGGGTC
 ACTGGGCGCAGGATGTGCTGCTACCGGCTACAACAAGACCGGCTTCTGCTGAGCAACCTCCCTCATCTGAC
 ACCACAGCAGGAGAGACTCAGCGACTACCGCTCATGGCGGACGATGGGTTGGGCGAGCCGGGCGAGCGGCTGT
 ATCTCTACAATGTCCAGTGTTTGAACCCCTTGAGGTCAACATGAGTATCCGAGTGTCTATCCCTGCGG
 CAGAGTGGCCAACTTACCTGTGAGGTGCGTGGGAACCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
 CTCTATCCAGCCAGCGGCTCTCGGCTTCTCCCGAGGGCCCTGCGCTGCTCAGCATGGGGCTGAGGACGAAGGC
 GTCTACAGTGCATGGCCAGTACAGGATTTGGGAGCGCCCATGCGGTAGTCTCAGCTGGGACCTTCAGGCCAAGC
 ATAAACCAAGGCTATGGCAGGATGCTGAGTGGCTACTGGCACAACCTCTGTATCACCTTCAAACCTCGGCAAC
 CTTGAGCAGATGCTGAGGGGGGCAACCGCGCTCCAGAGCCCAACGTCTGAGTGGGGCTGCTTCCCCAGAGTGT
 CCAGGAGAGAAGGGGCGAGGGGCTCCGCGGAGGCTCCCATCATCTCAGCTCGCCCGCAGCTTCCAGAGAGCT
 TCATATGAACTGGTGTGGCGCTCGGATGAGGGCAGTGGCCGGGCGCCAACTCTCTACTATGGTGAACAC
 CCAAGCAGGTCACAAATCTCTCTGACGATTGGACATCTCTGGCATTCAGGCCAACAGCAGCCGCTGACCTCT
 ACCAGACTCTCCCGCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAATCTCGGGGAGGGGCGAGACAGCC
 ATGGTCACTTCCAGACTGAGCGGCGGCCCAACCGGATCATGGCCAGCAAGAGCAGAGTCCAGAGAGC
 GACCTTGAGGCCAGTCCCGAGCAGCAGCCAGCCAGACCAGCGGCCCTCTCCCGCCAGAACTCCCGACAGG
 CCCACCATCTCCAGCGGCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCGTGGGAATGGTGGGTGCCAATC
 CAGTCTCTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACAGCGGCCATCCCCCA
 TCGCGGCTGCTCGGTGAGATCACGGGCTAGAGAAAGGCACTCTACAAGTTCCAGTCCGGGCTGTGAACATG
 CTGGGGGAGCGCAGGACCGGCCCTCTCGGCCCTACGTGGTGTGGGCTACAGCGCTCGCTGTACGAGAGG
 CCGGTGGCAGGCTCTTATATCACTTCAAGGATCGGCTCAATGAGACCACCATCATGCTCAAGTGGATGTACAT
 CCAGCAAGTAAACAACACCCCAATCCATGGCTTTTATATCTATTATCGAACCACAGCAGTGCAGATGATAGT
 GACTACAAGAAGATATGGTGGAAAGGGGACAAGTACTGGCATCTCAGGCCACTCAGGCCAGAGACCTCTCAT
 GCATTAAGATGCACTGTGTATGAGGAGGGGAGAGCGAGTTCAGCAACGCTGATGATCTGTGAGACCAAAAGCT
 CGGAAGTCTCTCGCGAGCTCTGTGACTGCCACCCCACTCTGCGCCACACAGCCGCTCTCTCTGAAC
 ATAGAGCGCGCGTGGGCACTGGGCGCTGGTGGCTCGCTCAGCAGCTGCCCCATCTGATTTCTGGGCTGCT
 CTGGGCTCCATCTGTTCTATCATCTGCTACCTTCACTCCCTCTGCTTGTGGAGGGCTGGCTTAAGCAAAACAT
 ACAACAGCCTGGGTTTCTCGAAGTGCCCTTCAACCTCTCGCCGTATCATATGTTGGTGCAATGGGAGCACTC
 CAGGCCACACGAGCCAGTGGCAGAGCCTTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCAGAT
 AATAGGGGCTGCCCTCGACTGGCTGGGCTACCGGCGCATGAAGCCAGCAGCACTGCCAGGGCGAGCTTCAG
 CAGCAGAGTGACACACAGCAGCTGCTGAGGACAGCCATCTTGGCAATGGATATGACCCCAAAGTCAACGATC
 ACAGGGGCTCCCAAGTCTAGCCCGGAGGAGGCTCTTTCTTATACACACTGCCCGAGCACTCCACTCACCGCTG
 CTCGAGCCCATCAGCACTGCTGCCACGCGCAGGAGCAGCTGCTGCTGTGGGCGAGTGGGGGTGAGGAGAGCC
 CCGACCTCTGCTTGGAGCACTGTGGAGCCCTTCATTTCACTCAGGCGCCGATGCTGCTTGGGCTTGTG
 CAGTGTGAAGCTGAGCAGCTCTGACTCTGCCAAGTCTGGGAGAGCACTGGTGTCCCGCAGCAGCCGTAGGG
 GCTCACTTAGCAGAGCACTGGAATGCAGCTCTCCCGGGCGAGTGGGCTGCTTTTGAACACACCT
 CTCACATTTAGGACGAAGCTGATATCCAGAAAGCATATATGTTTTTTTTAAAAAAAAGAAGAAAAA
 AGAGACAGAGAAAATGGATATTTATTTTCTATTATAGCCATATTTATATATTTAGCATTTGAAATAAATGTA
 TATGTTTATATTTCTGGAGAGACATAGGAGTCTACCGTTGAGGTGGAGAGGAAATAGAGCACTGCCA
 CTTAACAGAGGCTCAACCAGGAAGACACGACAGGCTGGCGGGAGAGACTCTTAACCTGGGGCTCTGTGAGT
 CGAGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAGAGTCCAGGACATGGTTATCACAGAGCA
 TGAGGGAACAGCAAGGGGCGAGGATATCACAGCTGGAGACACCCACACAGATGGCTGGATCCGGTGTCTACGGAA
 ACATTTTCTAAGATGCCATGAGAACAACCAAGATGTGACAGCACTATGAGCATTAAGAAACCTTCCAGAA
 CAATAATCCGTGGCAACATATCTCTGTAACCAACCACTGTACTTCTAATAATATGTTTAGTCTTCCGTGTA

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FIGURE 36

MLRGTMTAWRGMREVTILACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP
 RMNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPPSGNLQ
 IVNASQDEDEGMKYCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARIYPPEAQTIIIVTKGQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNVQVFEPPEVTMELSQLVI PWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLS
 RRALRVLSMGPEDEGVYQMAENEVGSAAHVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTS SVGPASPKCPGEGKGQGAPEAPIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRGTGRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRNGGFP IQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNT
 PIHGFYIYRPTSDNDSDYKKDMVEGDKYWH SISHLPQETS YDIKMQC FNEGGESEFSNMV
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL
 IIVTFIPFCLWRWSKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTL PDDSTHQLLQPHHDC CQRQE QPAAVGQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCGLGVPEEVDSPDSCQVSGGDWC PQHPVGAYVGQEPGMLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC
 CCAGGCTCCCGCGCGCGACCCCGCGCAAC**ATG**CAGCCACGGGCGCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTGCTCTGCTACTGCTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGGAGACCAGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGCTCCCCC
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCCCTCACTACGCCAGG
 CACCCCCAAAACCTTGGACCTTCGGGGTCGCGCGCAGGCCCTGATGCGGAGTTTCCCACTCG
 TGGACGGCCACAATGACCTGCCCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGGACCAGACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCTCCTACTCTGAACCTCGAGCTT
 GTGACCTCAGCTGAAGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTCTATGTGCTGGGGTGCGCT
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTCCACCAAGTTTCAGACAC
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCCCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG
 TTGAATGTTCGGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT
 GTCCATGGGGGTGCTGCAGTGCACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTTCATCGGGATTGGTGGAATATGACGGGACT
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCTTCGTGGAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT
 CCATATGGGCAACTGAGCACATCTGCCACTCCACCTCGTGCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCGTGGAGGTCCCTCAAATGCT
 CCCCATACTTTGTTCCAGGCCCTGTGGCTGCTGCCACCATCCCAACCTTCACCAGTGCGCTC
 TGCT**TCG**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT
 AGTTCATTACAAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

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FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
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ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLNRFSHGQ
TSLDRLRDGLVGAFWSASVSCSQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFFYQGLSTSC
SHLVPPQNGHQATHLEVTKQPTNRPVWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:

Signal peptide:

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristoylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGCATG
AAGCTCTTATCTTTGGTGGCTGTGGTCGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA
GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA
TTTACAACCAGAATGTATCCAGAAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
GTGCCTGGCCATGACGTGGAGGCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG
CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
AGGTGCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGCTTAGATGGGCTGG
TGTGGTTGGGTCAAGGCCCAACACCATGGCTGCCAGCTTCAGGCTGGACAAAGCAGGGGG
CTACTTCTCCCTTCCCTCGGTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCTCCTCT
CTCCCTAACTTTAGAAATGTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT
GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG
CCGCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCTTGAAGATAAAGCTGGGTCTTCA
GGAACTCAGTGTCTGGGAGGAAAGCATGGCCAGCATTAGCATGTGTTCTCTTCTGCAGTG
GTTCTTATCACCACTCCCTCCCAAGCCCCGGCGCTCAGCCCCAGCCCCAGCTCCAGCCCTG
AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCCTGGA
AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT
CTGCTGCCGTCCCCCTACCTGCACTTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTC
CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
CACCACAGCCCCGTGACTTGGGTGCCTCTTGTCCCTGAACCTTCGTTGTACCACTGCATGGA
GAGAAAATTTTGCCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG
TTTTATTCTCTCA

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FIGURE 40

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278

<subunit 1 of 1, 183 aa, 1 stop

<MW: 20574, pI: 6.60, NX(S/T): 3

MKLLSLVAVVGCLLVPPAEANKSSDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
FVPGHDVEAYCLCECRYEERSTTIKVIIIVILSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGSGTCTCGCTTGGGTTCCGCTAATTCTGTCTGAGGCGTGAGACTGAGTTCATAGGGTCCTGGGTCGCCGA
 ACCAGGAAGGGTTGAGGGAACACAATCTGCAAGCCCCCGACCCCAAGTGAGGGGGCCCGCTGTGGGTCCTCCC
 TCCCTTTGCATTCCCACCCCTCGGGCTTTCGCTCTTCTGGGACCCCTCGCCGGGAGATGGCCCGCTTGATG
 CGGAGCAAGGATTCGTCCTGCTGCTCTCTACTGGCCGCGGTGCTGATGGTGAGAGCTCAGAGATCGGCAGT
 TCGCCGGCCAAACTCAACTCCATCAAGTCTCTGTGGCGGGAGACGCCTGGTCAGGCCCAAATCGATCTGCG
 GGCATTGACCAAGGACTGGCATTCGCCGGCAGTAAGAAGGGCAAAAACCTGGCGAGCCCTACCTTGATAGACT
 GATAAGGATGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATCGGCCTGCATGGTGTGTCGGAGA
 AAAAAAGAGCGCTGCCACCGAGATGGCATGTGCTGCCCAAGTACCCGCTGCAATAATGGCATCTGTATCCAGTTC
 ACTGAAGAGCATCTTAACCCCTCACATCCCGGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAACGGTCATTAC
 TCAAAACCATGACTTGGGATGGCAGAACTAGGAAGACCACACACTAAGATGTCACATATAAAAGGGCATGAAGGA
 GACCCCTGCCTACGATCATCAGACTGCATTGAAGGGTTTTGCTGTGCTGCTGCTTTCTGGACCAAAATCTGCAAAA
 CCAAGTGTCCATCAGGGGGGAAGTCTGTACCAAAACACGCAAGAAGGGTCTCATGGGCTGGAATTTTCCAGCGT
 TGCAGCTGTGCGAAGGGCTGTCTTGCAAAAGTATGAAAGATGCCACCTACTCTCCAAAGCCAGACTCCATGTG
 TGTGCAAAAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTGATTTAATGCATTATAG
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 AAAGGGAGAAAGAAAAATGAACCTGAATAGATTAGAATGGGTGACAAATGCAGTCGACGCCAGTGTTCATTATG
 CAACTTGTCTATGTAATAATGTACACATTTGTGAAAAATGCTATTATTAAGAGAACACAGCACACAGTGGAAATT
 ACTGATGAGTAGCATGTGACTTCCAAAGAGTTAGGTGTGCTGGAGGAGAGGTTTCCTCAGATTGCTGATTGC
 TTATACAAAATAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAAATACTCTAGAAATAACTTGTTA
 TACAATAGGTTCTAAAAATAAAATGTCTAAACAAGAAATGAAACATGGAGCATTTGTAATTTACAACAAGAAAT
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 TTCAGATTCTACGGAATGCAGTATATCTCTTTATCCTATGTGATTCTCTGCTCGAATGCATTATATTTTCCAA
 AACTATACCCATAAAATTGTGACTATGATAAAATACCTACACAGAGCAGAAATTTACAGAGTCAAAAAAATTTTAAA
 GATGTCCAATATATGTGGGAAAAAGAGCTAACAGAGAGATCATTTATTCTTAAAGATTGGCCATAACCTATATTTT
 GATAGAATTAGATTGTAATAACATGTATTACATACACTCTGTGGTAATGAGACTTAAGCTGGATCTGTACTG
 CACTGGAGTAAGCAAGAAAAATTGGGAAAACTTTTCGTTTGTTCAGGTTTTGGCAACACATAGATCATATGTCTG
 AGGCACAAGTTGGCTGTTCATCTTTGAAACCAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTTGCTAT
 CATATAATTTACTATGCAGATGAATTCAGTGTGAGGTCTCTGTGTCGCTACTATCCTCAAAATTTATTTATTTATAG
 TGCTGAGATCCTCAATAATCTCAATTTACAGGAGGTTTCACAAAATGTACTCCTGAAGTAGACAGATAGTGAGG
 TTTCAATGCCCTCTATAAGCTTCTGACTAGCCAATGGCATCATCCAATTTTCTCCCAAACCTCTGCAGCATCTG
 CTTTATGGCCAAAGGGCTAGTTTCGGTTTTCTGCAGCCATTGCGGTTAAAAAATAAAGTAGGATAACTTGTAAA
 ACCTGCATATTGCTAATCTATAGACACCACAGTTCTCAAAATCTTTGAAACCACTTTTACTACTTTTTTAAACTT
 AACTCAGTTCTAAATACCTTTGTCTGGAGCACAAAACAATAAAAGGTTATCTTATAGCTGTGACTTTTAAACTTTG
 TAGACCACAATTCACTTTTAGTTTTCTTTTACTTAAATCCCATCTGCAGTCTCAAAATTTAAGTTCTCCCGATG
 AGATTGAGTTTGAGCGCTGTATATCTATTAAAAATTTCAACTTCCACATATTTCAATTAAGATGATTAAAGACTTA
 CATTTTCTGCACAGGCTGCAAAAACAAAAATTTATAAACTAGTCCATCCAAAGAACCAAGTTTGTATAAACAGGT
 TGCATATAGCTTGTGAATGAAATGGAACATTTCAATCAACATTTCTATATATAACAAATTTATATATTTTCAAA
 TTGGTTTCTGCAATATTTTCTTATGTGCCACCTTTTAAAAATTTATTTTGAAGTAATTTATTTACAGGAAATG
 TTAATTGAGATGATTTTCTTATAGAGATATTCTTACAGAAAGCTTTAGCAGAAATATTTTGCAGTATTTGAC
 TTTGTAATTTAGGAAAAATGTATAAAGATAAAATCTATTAAATTTTCTCTCTTAAAAACTGAAAAAATAAA
 AAAAAAAAAAAAAAAAAAAAA

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FIGURE 42

MAALMRSKDSSCCLLLLAAVLMVLESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
 FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNN
 GICIPVTESILTPHIPALDGTRHRDRNHGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
 SDCIEGFCCARHFWTICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
 SKARLHVCQKI

Signal peptide:

amino acids 1-25

TCTCAATCTGCTGACCTCGTGATCCGCGCTGACTTGTGAATCCACCTACCTTGGCCTCCCCAA
GTGTTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCAACATCAGCTTTTTAAAAATTGATT
TCTTCAAATTTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA
TAGCTGCATTATTATAGTCAGTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG
TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG
ATGTGTTTTAAAGCCTTGGGCAGAAATTCTGTATTGTTGAGGATTTGTTCTTTTATCCCCCT
TTTAAAGTCATCCGTCCTTGGCTCAGGATTTGGAGAGCTTGCACCACCAAAATGGCAACA
TCACAGCTCCCCAGTTTGGACAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC
CCAAGTACACAGCAGAATATGACCAAGTCACCTTACACTACTCTTCTTGGGACCTACAGCC
CCCAACATCCCAGTCCTCAGTCTCTCAGTACTTCTGACTTCAAATCTCAACTGAGCCATCCC
CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCTCCTCT
CCTGGTTTGGAGTCCTTTCTTCCCAGGCAAAACTTCGAGAATCAACACCTGGAGACAGTCC
CTCCACTGTGAACAAGCTTTTGACGCTTCCAGCAGCACCATTGAAAATATCTCTGTGTCTG
TCCACCAGCCACAGCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG
ATCCCAGCTTCTGCAGTGGAATGCCTGGTTACGAGATGTCACAGGATTAAATGTGCAGTT
TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG
AAAATAGTAATCAGATTCCCATCAGCTTGTATTGGAAGTCTTTAAGTGAGCCTTTGAATACA
TCTTTATCAATGACCAAGTCAGTACAGAACTCCACATATACTAACAATCCGCTATTACCTCCTG
CAGTCTCAGAAGCTCATCACTGAATTCGTAGTCCAGTACGAATGCTTCTCTCTTAGTACC
AGATTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCTCAGAGCTCAGCTFCCA
GGAACCATCATGAATGGACATGGTGGTGGTGAAGTCAGCAGACACTAGACAGTAAGTATAG
CAGCAAGCTACTCTTGTGTCATGGCTGGTGCCAACCAACAGGAAGAGGATAGCTCACGTGA
TGTGGA AAAACACCAAGTTGGTCAATGGCTCATTGTT**TAA**AAAGCAGCCCTTTTGCTTTTTTGT
TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
GGTGGTCTCATATTCTTCTGCCCTAATCAGACTGCACCACAAGTGCAGCATAAGTATGCAT
TTTTAAGATGCTTGGGCCAGCGGGGTGGCTGATGCCCATATCCAGTGCTTTGGGGGGCC
AAGGCAGGCAGATTGCCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAAACTG
TGCTCTTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGGCGGTGCCTGTAATCCCAG
CTACTTGGGAGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC
GTCTGAAAAAG

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FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT
PSTQQNSTSHPTTTTSSWDLKPPTSQSSVLSHLDFKSQPEPSFVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQFPQPKHIKLAKRRIPPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP
GTIMNGHGGGRSQOTLDSKYSSKLLLSWLVP TKQRKRIAHVMWKTPVGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC
 GTCCGCTGGAGGTACCGACGGCCCCCGGCCACCCCCGCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGGGCGCACCCGCGCTTCTGACCTGCGTGAACCGGGGCACGTGT
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCCTGGGACCGGCAGCCGCCGGG
 GTCCCGCAGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTGGGCGAGCGCCGCGCTA
 CGGGCCCCCTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTGACGGTCGCCGAACCCACGC
 GGAGCGCCCCCCCCGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCCAG
 ACCCCACACTGGCGCGCGGCCACAACGTCAATGTCATCGTCCCCGAGAGCCGAGCCCCAC
 TTCTTCCAGCAGCTGGGCTACGTGCTGGCCAGCTGCTGCTCTTTCATCCTGCTACTGGTTCAC
 TGTCTCTGGCGCCCCGAGCGCGCGGAGGCTACGAATACTCGGACCAGAAGTCCGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGCGAGTTCGCTGTGGCTGAGGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAATCCTGAAGGAGAGGGCGGAGCT
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGTTCCGGAAGGAGAACT
 GCAAATAGGGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC
 CTCGGGGCATCTCCTGATGCTCCGGGGCTCACCCCTTCCAGCGGCTGGTCCGCTTTCTCT
 GGAATTTGGCCTGGGCGTATGCAGAGGCCCTCCACACCCCTCCCCAGGGGCTTGGTGGC
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCACGGGTGGCCCTGCCACCCCTGGCACAACC
 AAAATCCCCTGATGCCATCATGCCCTCAGACCTTCTGGGCTCTGCCCCTGGGGGCTG
 AAGCATTTCTGGAGGACACTCCCATCAGAACCTGGCAGCCCCAAAATGGGGTCAGCCTCA
 GGGCAGGAGTCCCCTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCCT
 CCTCTGGGGTGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG
 GCACCATCTGTTCTCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGTCTCTGTGTTG
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTTCTCTGCCCATCCCTACCCTAGCCTTG
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTT
 GGACTCTGCTGGGCTGGAGTCTAGGGCTGGGGCTACATTGGGCTTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTGCCACTCTCAGACCCACATTT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCATCTGATTTTTAAAAA
 AAAAA

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FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWDRQPPGVPHDRADRLDL
YASGERRAYGPLEFLRDRVAVGADAFERGFSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPIRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSGKGDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLKDKFRKENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGGCGCTGGCGCAGCGGCGACATGGCCGTTGTCTCAGAGGACGACTTT
 CAGCACAGTTCAAACCTCCACCTACGGAAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTCAGCCTGGGCATTGGCAGTCTACTGCCATGGAACTTCTTT
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGGCCACCGGGGA
 GGACCCCTGAGGGCTCAGACATCTGAACTACTTTGAGAGTACCTTGCCGTTGCCCTCCACCG
 TGCCCTCCATGCTGTGCCCTGGTGGCCAACCTTCTGCTTGTCAACAGGGTGTGCAGTCCACATC
 CGTGTCTGGCCTCACTGACGGTCATCTGGCCATCTTCATGGTGATAACTGCAGTGGTGAA
 GGTGGACACTTCCCTCGGACCCGTGGTTTTTTGCGGTCACCATTTGTCTGCATGGTGATCC
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTTCTATG
 AGGAACTCCCAAGCACTGATATCAGGAGGAGCCATGGCGGGACGGTCAAGCGCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG
 CCACCATCTTCCCTCGTGCTCTGCATGGGACTCTACCTGCTGTCTCCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCTGTTCTTGGCGCCATGTGTTTTCTGGTGAAAGAGGAGCTTCCCA
 GGACTCCCTCAGTGCCCTTCCGTGGCCTCCAGATTCAATGATTCCACACACCCCCCTCTCC
 GCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTCACTACGTCTTCTTCATCAC
 AGCCTCATCTACCCCGCGCTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT
 GTGGACCACCAAGTTTTTCATCCCCCTCACTACCTTCCTCCTGTACAACCTTTGCTGACCTAT
 GTGGCCGGCAGCTCACCGCCTGGATCCAGGTGCCAGGGCCCAACAGCAAGGCCTCCAGGG
 TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTTCGTGCTCTGTAACATACAGCCCGCGCT
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAAGTCCCTGTG
 GGCTCAGCAACGGCTACCTCAGCACCTTGGCCCTCCTCTACGGGCCTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGCTCTTTATGTGTGCTTGGGCTTAACACTGGG
 CTCAGCCTGCTTACCCTCCTGGTGCACCTCATCTAGAAGGGAGGACACAAGGACATTTGGT
 CTTCAGAGCCTTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGGCCATGGAGGAAAGGCC
 TAAAGTTTCACTTGGGGACAGAGAGCAGAGCACTCGGGCCTCATCCCTCCCAAGATGCCA
 GTGAGCCAGCTCCATGCCATTCCGTGCAAGGCAGATATTCAGTCAATTAACAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA
 ACATTTCCACCTTTCTTAGCCCTTCAAAGATGCTGCCAGTGTTGCGCCTAGAGTTATTACA
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTCAGCT
 GACAGCGAGATGCAAGCAAATGCTCAGCTCTCCTTACCCTGAAGGGGTCTCCCTGGAATGGA
 AGTCCCCTGGCATGGTCACTCTCAGGCCCAAGACTCAAGTGTGCAAGACCAAGCCCTGTGTTCT
 GCGGGTGAACAACCTGCCCACTAACCAGACTGGAAAACCCAGAAAGATGGGCCCTCCATGAAT
 GCTTCATTCCAGAGGGACAGAGGGCTCCTCTGTGCAAGGGATCAAGCATGCTGGCCTGGG
 TTTTCAAAAAAAGAGGGATCCTCATGACCTGGTGGTCTATGGCTGGGTCAAGATGAGGGTC
 TTTCAAGTGTCTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC
 GTATTTAAAAA

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FIGURE 48

MAVVEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGQLQRPEDRFCGTYIIFFSLGI
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL
 LVNRVAVHIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI
 YGMTGSFPMRNSQALISGQAMGGTVSAVASLVDLAASSDVRNSALAFFLTATIFLVLCMGLY
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLAPSVASRFIDSHTPPLRPILKKTASLGF
 CVTYVFFITSLIYPVAVCTNIESLNKGSGLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
 305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCTGCTGTACCAAGAGCTGGAGACACCA
TCTCCACCAGAGAGTCAATGGCCCCATTGGCCCTGCACCTCCTCGTCTCGTCCCCATCCTCC
TCAGCCTGGTGGCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGAACCTGGGGGCTCAATCGGACCCCT
GAAGCCCCAGAGGGTGATTGTGGTTGGCGCTGGTGTGGCCGGGCTGGTGGCCGCCAAGGTGC
TCAGCGATGCTGGACACAAGGTACCATCCTGGAGGCAGATAACAGGATCGGGGGCCGCATC
TTCACCTACCGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCCTGGGGCTCAACCTGACCAAGTTCACCC
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
AAGTGGCCGAGAAGCTGGGCTACGCCTTGCGTCCCCAGGAAAAGGGCCACTCGCCCCAAGA
CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGGCTGCAGAAAGG
CGATGAAGAAGTTTGAAAGGCACACGCTCTTGGAATATCTTCTCGGGGAGGGGAACCTGAGC
CGGCCGGCCGTGACGTTCTGGGAGACGTGATGTCCGAGGATGGCTTCTTCTATCTCAGCTT
CGCCGAGGCCCTCCGGGCCACAGCTGCCTCAGCGACAGACTCCAGTACAGCCGCATCGTGG
GTGGCTGGGACCTGCTGCCGCGCGCTGCTGAGCTCGTGTCCGGGCTTGTGCTGTTGAAC
GCGCCCGTGGTGGCGATGACCCAGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
CCCGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
CGGTGAAGCGCATCACCTTCTCGCCGCCGTGCCCGCCACATGCAGGAGGCGCTGCGGAGG
CTGCACTACGTGCCGGCCACCAAGGTGTTCTTAAGCTTCCGACGGCCCTTCTGGCGCGAGGA
GCACATTGAAGGCGGCCACTCAAACACCGATCGCCCGTCGCGCATGATTTTCTACCCGCCGC
CGCGTAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTGGACGCGGCGGCAGCGTTTCGCC
GGCTTGAGCCGGGAAGAGCGGTTGCGCTTGGCGCTCGACGACGTGGCGGCATTGCACGGGCC
TGTGCTGCGCCAGCTCTGGGACGGCACCGGCGTCTGCAAGCTTGGGCGGAGGACGACACA
GCCAGGGTGGCTTTGTGGTACAGCCGCCGCGCTCTGGCAACCGGAAAGGATGACTGGACG
GTCCCTTATGGCCGCATCTACTTTGCCGCGGAGCACACCGCCTACCCGCACGGCTGGGTGGA
GACGGCGGTCAAGTCGGCGCTGCGCGCCGCATCAAGATCAACAGCCGGAAGGGGCGCTGCAT
CGGACACGGCCAGCCCCAGGGGCACGCATCTGACATGGAGGGGCAGGGGCATGTGCATGGG
GTGGCCAGCAGCCCCTCGCATGACCTGGCAAAGGAAGAAGGCAGCCACCCTCCAGTCCAAGG
CCAGTTATCTCTCCAAAACAGACCCACACGAGGACCTCGCATTAAAGTATTTTCGAAAAA
AAA

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FIGURE 50

MAPLALHLLVLPILLSLVSQDWKAERSQDPFEKCMQDPDYEQLLKVVVTWGLNRTLKPQRV
IVVGAGVAGLVAACKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKVPEKLGALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDVMSEDDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLPRALLSSLSGLVLLNAPVVAMTQGPHDVHVQIETSPPARNL
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRRLHYVPATKVFLSFRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLASYTWSDAFAAGLSREEALRLALDDVAALHGPVVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHGVAASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCGGCCCTTGCTGCCTGCAT
 GGACGCTCTGAAGCCACCCCTGTCTCTGGAGGAACCCAGAGCGAGGGAAGAGGACAGGAGCTCGTGTGGCAGGAA
 GAATCAGAGCGCGGGAAGCCCCCATCTACTAGAAGCACTGAGAGATCGCGGCCCTCGGAGGGTCTGAATTTCTCT
 GCTGCTGTTTCACAAAGATGCTTTTATCTTTAACTTTTGTCTTCCCACTTCCGACCCCGCGTGTGATCTGCAT
 CCTGACATTTGGAGCTGCCATCTTCTGTGGCTGATCACCAGACCTCAACCCGCTTTACCTCTTCTTGACCTGAA
 CAATCAGTCTGTGGGAATTGAGGGAGGAGCACGGAAGGGGTTCCCAAGAAACAAATGACCTAACAAAGTTGCTG
 CTCTCTCAGATGCCAAGACTATGTATGAGGTTTCCAAAGAGGACTCGCTGTGCTGATGACCAATGGGCCCTGCTTGGG
 ATATAGAAAACCAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGACAGAGTACCTGGGTTTC
 CTGTCTCTTCATAAAGGTTATAAATCATCACCAGACCACTTTGTGCGGCATCTTTGCTCAGAANTAGGCCAGAGTG
 GATCATCTCCGAATTTGGCTTTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTTTGGGACCAGAGC
 CATCGTACATATTTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACCCCAAAAGGCAATTTGGTGTCTAG
 AGGGAATTGATAGAAAAGGCTTACCCTGAGGCTGAAGGTGATCATCTTATGACACCTTTGATGATGACCTGAA
 GCAAAGAGGGGAGAGAGTGAATTTAGATCTTATCCCTATATGATGCTGAGAACCTAGGCCAAAGAGCACTTCAG
 AAAACCTGTGCCCTCTAGCCAGAAAGACCTGAGCGTCATCTGCTTACCAGTGGGACCACAGGTGACCCCAAAGC
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCTTCTCAAATGCTGGAGCATGCTTATGAGCC
 CACTCTGATGATTTGGCCATATCTACCTCCCTCTGGCTCATATGTTTGAAGAGGATTTGACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTTGGATTCTTCAAAGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC
 CACATTTGTTCCCGCGGTGCTCGACTCTTAAGAGGATCTACGATAAGGTACAAATAGGCCCAAGACACCTTT
 GAAGAAGTTCTTGTTGAAGCTGGCTGTTTCCAGTAATTTCAAAGAGCTTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTTGCAAAAGATCCAGGACAGCTTGGCGGGAAGGGTTCGTGTAAATTTGCTCATGGAGC
 TCGCCCATGTCTCACTTCACTCATGACATTTCTCCGGGACGCAATGGGATGTCAGGTGTATGAAGCTTATGGTCA
 AACAGAAATGCACAGGTTGGCTGTACATTTACATTTACCTGGGGAAGTGGACATCAGGTGACGTTGGGGTCCCTTGGC
 TTTGCAATTAAGTGAAGCTGGAAGATTTGGCTGACATGAACACTTTACAGTGAATTAAGGAGAGGCTGCTCAT
 CAAGGGTACAAACGTTGTTCAAAGGATACCTGAAGGACCTGAGAGACACAGGAAGCCCTGGACAGTGTATGGCTG
 GCTTCACACAGGAGACATTTGGTCTGGCTCCGGAATGGAACCTTGAAGATCATCGACCTAAAGCAACACTTTT
 CAAGCTGGCCCAAGGAGATACATTTGACACAGAGAAGATAGAAAATATCTACACAGGAGTCAACCAAGTGTACAA
 AATTTTGTACAGGGGAGAGCTTACGGTCATCTTACGGTCACTTTAGTAGGAGTGGTGGTCTTGACACAGTATCTTCCCTC
 ATTTTGACGCCAAGCTTGGGTGAAGGGCTCCTTTGAGGAACCTGTGCCAAACCAAGTTGTAGGGAAGGCCATTT
 AGAAGACTTGCAGAAAATTTGGGAAAGAAAGTGGCCTTAAACTTTTGAACAGCCCAAGGCCATTTTCTCATCC
 AGAGCCATTTTCCATTGAAAATGGGCTTGTGACACCAACATTTGAAAGCAAGCGAGGAGAGCTTCCCAATACTT
 TCGGAGCCAAATTTGACAGCTGTATGACACATCCAGGATTAGGATAAGGTACTTAAGTACCTGCCGGGCCACTG
 TGCATGCTTGTGAGAAAATGGATTAAAACTATCTTACATTTGTTTGGCTTTCCCTCTATTTTTTTTAAACC
 TGTTTAAACTCTAAAGCCATAGCTTTTGTGTTTATATTAGACATATATGTGAAGTGTAGTTCCCAATAAATCA
 ATCTGTGTTTCCCATCTTCGATGTTGCTAATATTAAAGCTTCCAGGCTACTTTTATCAACATGCCTGTCTTCA
 GATCCAGCTTTATGTTCTGTGTCCTTCTCATGATTTCCAACTTAAATCTATTAGTAAACCAAGCTTCAAGGGT
 CAAAGGGACCTCTGTGCTCTTCTTCTTGTGTTTGTGATAAACATAACTTCCCAACAGTCTCTATGCTTTATTACA
 TCTTCTACTTGTCTTCAAATCAAGAGTTTAAATTTCTGAAAACCTGCTTCAACTCATGTTTCTAGCACTTATTTA
 CAACCACTAAAAATTTAGTTTGTAGCTTATCACTCATGTCAATCATATCTATGAGACAAATGTCTGAGTGTCTT
 CTGCTATAATTTAAATTTGTGACTGAAGGGAAAGTTTGTATCATACCAACATTTCTTAACTCTCTAGTATGATA
 TCTGATTTGGGAGTATTAAAAATGGGTCTATGACATCTGTCCAAAGGAATGCTGTTCTTAAAGCAATTTTAA
 CAGTAGGAACCTGGGAGGATAACTGCTCCCTACAGTTTGTGCTGAGCTGGAAGTGGGGGAGGAGGTGACAA
 GGTGGGCGGAGTGAACCTTTCCAGTAAATGAAGCAAGCACTGAATAAAACCTCTGTAACCTGGGAAACAAAGATCT
 ACAGGCAAGACAGATGCCACACAAAGGCTTATTTCTGTGAAGGAACACTGATCTCCCCACCTTTGGATT
 AGAGTTCTCTGCTTACCTTACCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC
 TATTACAGATAAAAAA

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FIGURE 52

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775

<subunit 1 of 1, 739 aa, 1 stop

<MW: 82263, pI: 7.55, NX(S/T): 3

MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFFLLFTKMLFIFN
FLFSPLPTPALICILTFGAIFLWLI TRPQPVLP LLDLNNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVII LMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNI VSNAAFLKCEVHAYEPTPDDVAISYLP LAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNEAKTPLKKFLLKLA
VSSKFELQKGIIRHDSFWDKLIFAKIQDSLGGVRVIVTGAAPMSTSVMTFFRAAMGCQVY
EAYGQTECTGGCTFTLP GDWTS GHVGVPLACNYVKLEDVADMN YFTVNNEGEVCIKGTNVFK
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLQIFVHGESLRSSSLVG VVPD TDVLP SFAAKLG VKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPF SIENGLLTPTL KAKRGELSKYFRTQIDSLYEHIQD

Important features:

Type II transmembrane domain:

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGCGGAGGCCGCGGCGAGCCGGGCGGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCCGGGGGCCCTAAGCCATTCTCGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT
 CCGGTATGGACGACTGGAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAAGCGG
 AGCTGGTACCTTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA
 GACAGGGGCGGTGCTTTTCTGCTGGTGACTGTCAATTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGAGCCATCAGTGAAGCCAAATGAAGACCCAGAGCCAGACGAAGCATATGATGAGGCC
 CTAGGCCGCTTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG
 AGGCCCGGGAGCAGGGCCGGGGCATCCATGTCTATTGTCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAACGTTGTGTTGACACGTACTACCTCATGAGGATGAGGCCATGGTGCTATTCTCT
 CAACATGGTAGCGCCCGGGCAGTGCTCATCTGCACGTCAAGGATGAGGGCTCTCTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGGCCCTGGGC
 TGGAGGGACACATGGGCGCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATTCT
 TAAGTCACTGCCCTCTCTTCTTGGGGGACCCAGTCTCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAGAAGGACGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCGCCGGCGC
 TTCTGCAGCAAAGTTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCTCAATGTGCGTGTGGCTGTCTATTGACG
 GGAACCGACCCAAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTACGCCACGGGGGTGTCT
 CCTCAGATGATAACGATTTTCTATTGACGGCTACTATGAGGAACCCATGGATGTGGTGACCT
 GTTTGGTCTGAGGGGATCCAGCATACTCCCATCAGCATCAAGAATGCCCGGTGTCTCAGC
 GTTACAAGGCCAGCCTCACTGCCACTTTCAACCTGTTTCCGGAGGCCAAGTTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTTTCAGTTTCCGTGAGGCAATCCATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCTGGAATGACACAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTACTGTACCGGTGTGGAGACCATGCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCAAAGTGGCCTACACCGGAAAAGCTCTGGGA
 TTGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGCATCATCCCTGACG
 TTTCGGATCTTACCATTTTGGCATCGCTCGGCCCTCAACATGAATGGCTACTTTCACGAGGCC
 TACTTCAAGAAGCACAAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGCTCT
 GAAGAAAAGAAGCTTATGAAGTGGAAGTTTCAAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC
 ACAGCAAGAACCCTTGTGAAGACTCTTCTTCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTGCAATGGAGAAAGATGATGACTTCAACACCTGGACCCAGCTTGCCAAGTGCCCTCCA
 TATCTGGGACCTGGATGTGCTGGCAACCATCGGGGCTGAGGCTGATTTTCGGAAGAAGA
 ACCATTCTCTGGTGGTGGGGGCTCCGGCTTCCCTCTACTCAGTGAAGAAGCCACCTTCAGTC
 ACCCAATTTTCTTGGAGCCACCCCAAGGAGGAGGGAGCCCAAGAGCCCGGAGAACAGAC
ATGAGACCTCTCTCAGGACCTTGCGGGGCTGGGTACTGTGTACCCCCAGGCTGGCTAGCCCT
 TCCTCCATCTGTAGGATTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTAACTA
 TGAGACTTAATTACTAATCAAGGGGAGGTTTCCCTGCTCCAACACCCCGTCTGTGAGTT
 AAAAGTCTATTTATTTACTTCTTGTGGAGAAAGGGCAGGAGAGTACTTGGGAATCATTAGC
 ATCCCTAGACGCTCATCTGCCCTTTGAATACCCCTCACTTTACAGGCTGGCTCAGATCTA
 ACCTATTTATTGACTGTCTGAGGGCCTTGAAAACAGGCCAAGCTGGAGGGCCTGGATTCT
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAAGCTGCTGTGCC
 CAACCCATGGACAGGCCACGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCCTA
 GACACTGGACAGGCCCTCTCTCAGCCTTCTCTTGTCCAGATTTCCAAGCTGGATAAGTT
 GGTCAATTGATTA AAAAAGGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 54

```
></usr/seqdb2/ss/t/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop .
><MW: 75220, pI: 6.76, NX(S/T): 0
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RAISEANEDPEPEQDYDEALGRLEPPRRRSGSPRRVLVDVEVYSSRSKVYVAVDGTTVLEDEA
REQGRGIHVIVLNLQATGHVMAKRVEVTSYPHEDEAMVLFNLNMPAGRVLICTVKGDEGSHFLK
DTAKALLRSLGSGAGPALGWRDTWAFVGRKGPGVFGEKHSKSPALSSWGDVPLLKTDVPLSS
AEEAECHWADTELNRRRRRRCFSKVEGYGSCVCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNYLRLMLRSLLSAQGVSPQMIVTFIDGYEEMPMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPEAKFAVVLEEDLDIAVDFFSFLSQSIHLEEDDSLICYISAWNDDQGYEHTA
EDPALLYRVETMPGLGWVLRLRSLYKEELEPKWPTPEKILWDWMMWMPQRRGRCEIIPDVS
RSYHFGIVGLNMGNGYFHEAYFKKHKFNTPGVQLRNVDSLKKEAYEVEVHRLLEAEVLDSH
KNPCEDSLPMDTEGTYHVAFIRMEKDDFTTWTQAKCLHIWDLVDRGNHRGLWRLFRKKNH
FLVVGVPASPYSVKKPPSVTFIPELPPKEEGAGPEAT
```

Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACTGGAAAGCCCACTCTCTTGGAAACCACACAC
 CTGTTTAAAGAACCTAAGCACCATTAAAGCCACTGGAATTTGTTGTCTAGTGGTTGTGGGTGAATA
 AAGGAGGGCAGAAATGGGATGATTTTCATCTCCATTAGCCTGCTGTCTCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTTCCCTTGGCTGTTAAATTTCTCAGAGGAACGACTGAAGCTGGTGACTGTTTTGG
 GTGCTGGCCCTTCTCTGTGGAACCTGCTCTGGCAGTCATCGTGCCCTGAAGGAGTACATGCCCTTTATGAA
 GATATTTCTGAGGGGAAAACACCACCAAGCAAGTGAAACACATAAATGTGATTGTCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCAGCCACGACCACACACAGCTGCATGCCCTATATTTGGTG
 TTTCCCTCGTTCTGGGCTTCGTTTTCATGTTGCTGGTGGACCAGATTGGTAACCTCCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGCTAGCAATTCCAAAATCACCACACCGCTGGGTCTGGTTGTGCCA
 TGCTGCAGCTGATGGTGTTCGTTTTGGGAGCAGCAGCATCTACTTCCACAGCAGCTGCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTTCCCTCTTGATGCATGCT
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCTATTGGCAGCACCAGTTATGTCCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTTCAGAGGTGAACGCCACGGGAGTGG
 CCATGCTTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGGCGGA
 ATAGGGCAGCAGCCACAAGCCCGATGCCACGGGAGGGAGGCCCTCAGCCGCCCTGGAAGTGGCAGCCCT
 GGTTCCTGGGTTGCCCTCATCCCTCTCATCTGTCACTAGGACACAGCATTAATGTTCAAGTCCAGC
 CTTGGTCCAGGGCCGTTTGGCAGCTCAGTGAGAACAGCCGGCAGCTGCAGACTACTCACTTCTCCACGT
 TCTTGTCTCACTTGGCGATCTCTACATGTATTCTTAGAGTCCAGAGGGGAGGTGAGGTAAAAACCTG
 AGTAATGGAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTGTGT
 TATCTTTTAAAGGCCCTTGACATTTTGGCTTTTAATATTTCTTTAACCCATTTCTCAGGGAAGATG
 GAATTTAGTTTAAAGGAAAAGAGGAGAACTTCATACTCACAATGAAATAGTGATTATGAAATACAGT
 GTTCTGTAATTAAGCTATGTCTCTTTCTTCTTAGTTTAGAGGCTCTGCTACTTATCCATTGATTTTT
 AACATGGTTCCCAACATGTAAGACTGGTGCTTTAGCATCTATGCCACATGCGTTGATGGAAGGTGATA
 GCACCCATCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTCTTTATATCAAAAGAGATATCCATTGAAAGGGGATGTTAGAGGGATT
 TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCTGCCATTCATCAATGAGCAGGAGAGG
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCTTGTCAGTTCTCCTTTGCGAAT
 AACTGTCTCCACATTCCTAGAGAGGAGCCAAAGTTCTAGTAGTTTCAGTTCTAGGCTTCCCTCAAGAA
 CAGTCAGATCACAAGGTGTCTTTGGAAATTAAGGGATATTAATTTTAAGTGATTTTGGATGGTTAT
 TGATATCTTTGTAGTAGCTTTTTTAAAGACTACCAAAATGTATGGTTGTCCTTTTTTTTTGTTTTT
 TTTTTTTTTAATATTCTCTTAGCAGATCAGCAATCCCTCAGGGACCTAAATACTAGGTCAGCTTT
 GGCACACTGTGCTTCTCACATAACCACCTGTAGCAGATGGATCAATAAGAGAAGTGTTCGCTA
 TGTATTAAAGCTTATTGGAATCATGTCTCTTGTCTCTCGTCTTTTCTTTGCTTTTCTTCTTAACCTT
 TCCCTCTAGCCTCTCCTCGCCACAATTTGCTGCTTACTGCTGGTGTTAATATTTGTGTGGGATGAAT
 TCTTACAGGAACCACTTCTCGAACTGTAATAAGATAATAATATCTTTATCTTTATCCCCCT
 CAAAGAAATTAACCTTTGTGTCAATGCGCGCTTTGTTGAGCCCTTAAATACCCACTCCTCATGTGTA
 ATTTGACACAATCACTAATCTGGTAATTTAAACAATTAGATAGCAAAAGTGTTTAAACAGCTAGGATA
 ATTTTCTTTTCATATTTGCCAAAATTTTGTAAACCTGTCTTGTCAATAAAGTGATATAATATTGTAT
 TATTAATTTATTTTACTTTCTATACCATTTCAAAACACATTAACATAAGGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGACGTAGTAGTTTGTAAAAACGTTTTCTATGACGCATAAGCTAGCATGCTATG
 ATTTATTTCTCTCATGAATTTGTCACTGGATCAGCAGCTGTGGAAATTAAGCTTGTGAGCCCTGTCT
 GGCCACAGTGAGGAAAGTAGCAAAATAGGATACAGTTGTATGTAGTCATTGGCAACCAATTCATACA
 ATTTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCTTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGTTTCACTAGTCCTTCAAACTATATGGTTGCCTAGATTCTCTCGGA
 AACTGACTTTGTCAATAAATAGCAGATTGAGTGTCAAAAAA

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FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVDQ
IGNSHVHSTDDPEAARSSNSKITTTLGLVVHAAADGVALGAAASTSQTSLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPLILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

GCTCGAGGCCGGCGCGCGCGGAGAGCGACCCGGGCGGCTCGTAGCGGGCCCCGGATCCC
CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGTGATTTTGAGATGATGGGCTTGG
GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCCGCCCTGGTGGCTGCATC
ATCGTCTTTGGGCTTCAACTACTGGATTGCGAGCTCCCGAGCGTGGAACCTCAGACACGGAT
CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
AGAACGAGTTCCAGGGAGAGCTGGAGAAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTGGTGAA
TAACATCACCAAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
GGAATTACCGCAGGCTGCACAGGATGTCTCCAGATTTCAGAGAACCAGACCAACCTGGAG
AGGAAGTTCTCCTACGACTGACCGTAGCCATCAATCAGTAGAAGAGGTGAAGAACACTG
TGAGGAGCGAATAGAAGAGGTGACCAAAAGGGGAATGAAGCTGTAGCTGAGGACACTGA
GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
GCAGCAGGCTGCCACACACAGAGGTGAAACAAGGGAAGGGAACGTGCTTGGTAACAGCAA
GTCCAGACACCAGCCCCAGTTCGGAAGTGGTTTGGATTCAAAGAGACAAGTTGAGAAA
AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGACAGGCTGCCGAGGAG
CCAGGCGGGGAGCAGGTGGTGGGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCG
AGAACTGGGCCAGCCCCACAGGTGCAGGCTGCCCTGTAGTGAGCCAGGAAAAATCAGAGA
TGGAGGGCCCTGAGCGAGACCAGCTTGTCATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
GCCGGGAAGGGAGAAACCAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA
TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
TTTTTAATGCTTGAAGATCAGAAAAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG
AATCATACACTCTGAATTGAAGTTGAATCATCATATTTACACAGGCGGAGAGATGACTA
TAAAAATGTTTATCGAGGAGCTGAATCTGAAAACTGTGAATGTACTAAATAAAATGTACATCTG

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FIGURE 58

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVLDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNDRQQQLQALSEPQPRQLQAAGLPHTTEVPQGKGNVLGNSKSQTPAPSSSEVVLDSCR
QVEKEETNEIQVVNEEPQRDRLPQEPGREQVVEDRPFVGGRGFGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEQEAAGEGRNQQLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

FIGURE 59

CGATGCGAGAAAGCCCTCAGCTTGGCTCTTCTGGCCTGGGTCTGCTCTCTCTTCTACGCTGGCATTGCCTCTTCA
CCATGGGCTTCTCTGACCCCTTTGGAGCTCTACCAACCATGACGAGCTCGCAAGAGCCCCCAGGCCCTGGGTCCG
TGCCATTGGGGGAGCCAGCGAAACCTGGGGCTGCTGGATGGCTTCCCGATTTCGGGGGTGTGTGGTGTCTGA
TAGATGCTTCTGCATTTCCTCTGCCCGCCAGCATTCACAGCTCTCTAGAGAGCTCTCTGTTCTCCCTACCTCT
TCTTGGGCAAACTAACCTCTCTGACAGGATCTCTGAGATTTCAGCCACCATTGCCGGGTCTACGATCTCTCAGG
TGACCTCTCTACACACCATCTCAGGCGCTCAAGGCTCTCACCACCTGGCTCACTGCTACCTTTTATGTATGCT
GTAGTAACTTCGGCAGCCACCGGATGTGTGAAGAACATCTTAATGAAGACTCTACAGTCTCGAAGAGGCGGTAG
TCTCTATGSGAGATGATACCTGGAAGACATTTCTCCCTGGTCTTTCTTCCAAAGCTTTCTTCTTCCCATCTCT
ATGTACGACAGCTAGACACAGTGGACATGGCATCTGGAACCTCTACCCACCATGACAGTGGTGAATGGG
ACGTCGTCTGTCTCATCTCTGGGTGTGGACACTGTGGCAACAGTGGCCCTGAGGAATGACACCTGCTGAATGTTG
TCGGGACCATGGGATGACCAAAATGGAGACACTGAGGGAGACAGTGAAGTGTCTCAAGTCTGAGTCTCTCTTCT
TGATATCCCCACAGCTCTTCCCGACACCCACGAGGGAGCAGAGTGAATCTCTCAAGTTAGCTTTGTGTC
CCAGCTTGGCCTCTGCTGTGGGCTGCCCATCCATTGGGAATCTCGGGGAATGATGGCTGAGTCACTCTCTCAG
GGGCTGAGGACTCCGACCCCACTCTCTGTTTACCCACAGCTCAGCTCTCATCTCAATGCTACAGAGTTGT
TCGATTCTTTCATCTACTCAGCTCTACTCAGGACTCTCAAGCTAAGGAGCTCTATCAGCTCGACAGCTCT
TCTCAAGGCTCTGTCTGACTACAGTGGTCTTCCAGAGCCCAAGGGGCTGAGGCCAGCTCCGCAATCTGTA
TCTGCTGAGCTCAGCAGTCTCTGTGGGAGCTCGGGCACTGTGATCTCAGTCTTGGGCTGTTTCTCTGTCTTC
GATGCGGGGGGTGTGCTCTTCTGGCTCTGCTTCTGCTTATGCTGCTGTGAGCTCTCAGTGGGCAATATCCC
CAGGCTTTCCATCTTCTGCCCTCTACTCTTGACACTGTGGCTGGGCTGGTGTGGGCAATAGCGTATGCTGTGAC
TCTCGGAATCTTAGGCTGAAGCTAGATCTATGCTCTTAGGGGCTGTGGCTGAGCTGAGTCTATCTCCCTCTT
TCTGTGGAAGAGCTGGGCTGGCTGGGGGTCCAAAGAGCCCTGGCAAACTGTTTCCCATCTCTGGGCGCTCTC
TGTTATCTCTGCTGTTTCTTGGCTGTGTTTCTCTGTATGTTTCTTGTAGCTGAGGCAAGGCCACCCCTCT
TCTTTTGGGCTCATTCATCTCTGCTGTGTTGGCCAGTCTCAGTGGAGGCCAGCTGTTTCCACATAAGCTAT
TCACAATCCCGCTCTGGCATTCAGCCACAAACCCCAAGCCAAATGGTGATATCTCCCTGGAGGCTTG
GAATGGGTTGCTTATGTGTACAAGAGCTAGCTGGGCTTTTATCATGCTGCCCTGAAGAGACACCTGTTTGCACCT
CTTCTCTCTGCTGATGCTCTTGCACTCAATGCTGGGTTGTGAGCCAGCAAAATTTAGTATGGAGCTTGTGTGG
CCGCGCTGTGGGCTGTTAGTCTGCGTGGCTTGTGGCTTCCGCCATCTGTGAATCTCAAGAGCCCGACGACCA
CATGCTCTTGTGTGGCTGGGAGTGCCCTAATGCAATGGGTACTGCTGCTATCTGGGCATGGGCTGGGGG
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TGGCTGCTTCAAGGCTCCGGCTGTGCTCTGGAAGCTGTGACAGTGTGCTGTGAAGGCTGGGGAGCGGCTCCAA
GGACAGGAGCTGCTCATCTCCCTTCTCAGGCGCCCACTCTTCAAGCTCACTTGATTAATGTGGTCTCCATCAA
TCTACGACACATCAGGAGGAGTTTCGGGGCGGTGAGAGAGCAAAATCAGGGTCCCTGACCTGTGGCTCT
TCTATGACTGGGAGTGCTACTACGAGTCTATGTCACAGGCTCAACCTGTGGGCTTCCCACTTCTGCTGT
GTGATCGGGAGGAGCTAGCTGTTGTGTTCTGCTTCTGTTTCTGAGAGCTTCTCTCTCAATCTGTTCTGCT
CTGGATACCCGTCACACCCCTGGTCTTTTACTTGCCATGGGAGGAGCTCTCGGCTTGGGCTCTCATGGCCA
CAGACAGCTCTTACTTCCAGGCGCACAGGCTGCTTTTCAAGCCATCATTTGGATGACAGCTCTGTGGGATTC
CAGAGGCTCATGGCTCTGTAATCTGGCTGCTGCTTGTGATGTGGGAGCAACACCTTTGCTCTCCACCTCTCTCT
TTCAGTAGGTTGCCCATGCTCTGCTCTGCTCTGCTTCTGTTGTGAGAGTCAAGGCTCGGAAGAGACAGCAGC
CCCCAGGAATGAAGCTAGTCGAGAGTCAAGCCGAGGAGGAAGAGGACCTATGAGGATGAGTGGGCTCGGG
ATGGCTCTCAGCATCTTATGACGAGCTGCTCAGCTGGGCTCAAGTACTTATCTATCTTGGTATCAGATTT
TGCGCTTGCTCTGGCAGGCTCCATCTCTCGAGGATCTCATGTTCTGGAAGTGTGTGGCCCTTAAGTCTATAT
TGTAGGCTTGGGCTCTATGTGAGCGCTGGGACTCTCTCGGCACTGATTTGGTGAATGAGTGGATGGTG
CTGTGAGCTCTGTTCTCAGGCACTATTTCTGGCCAGCAGAGGAGTCTAGTCTGTGATTAATGAGCTTGCT
ACAGAGATGCTGGGAAGACAGTGTAGCTGGCTCTACAGTATGGATGATCGAAGCAGGCTCAGCCATCAT
TCTTACTATCATCAGCAGGAGGGCGCTGACATCTAGGACTCATTTATATTAATTCAGGACAGCAGTGGGAT
TGATCCCTAATCTCTATTTGGATGATCTGAGGACAGAGGGGGCGGTCTCGAAGTGGGAATAAATAGGCGCG
GGTGGTGAGTCTGACCTATAATCCGACAGTCTGGGAGCAGAGGTGGGAGATTTGTTGTGCTCCGAGAGTTCA
AGACAGGCTCTGGAACATAAAGACCCCGTCTTCACTTATAAAATAAGTGAATAAATGATATAAT

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FIGURE 60

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPGPGSLPWGSQGKPGACW
MASRFSRVVLVLIDALRFDAQFQHSHPREPPVSLPFLGKLSSLRILEIQPHHARLYRSQ
VDPPTTTMQRKLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMDDTWKDLF
PGAFSKAFFFPFSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIHFLGVHDCHGKHGPHHP
AKKLSQMDQVIQGLVERLENDTLLVVAGDHGTTNGDHGGDSELEVSALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHNAQ
QVSRFLHTYSAAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAIISPGFFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLFR
VFFSDSFVVAEARATPFLGSGFILLVVLHWEQQLLPKLLTMPRLGTSATNPPRHNGAY
ALRLGIGLLLCRLAGLFHRCPEETPVCHSSPWLSPPLASMVGGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPRLRLVLSGASMLP
RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHM
QEEFRGLERTKSQGPLTVAAYQLGSVYSAMVTALTLLAFPLLLHAERISLVFLLFLQSFL
LLHLLAAGIPVTPPGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWHAAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLLWPFLLCESQGLRKRQPPGNEADARVRPEEEEE
LMEMLRLDAPQHFYAALLQLGLKYLFIILGIQILACALAASILRRHLMVWVFAKPFIFEAVG
FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCTGT
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**AATGT**
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGGAAGAGAAATCCAGAAGACCTTCCTGTTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCGAACACTCTTTACTGCGT
 ACACGTGGAGTCCTTTCGTCCCAGGGCCCCCTCGCCGTGCTCAGCCTTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAATCATCTTCTGGTATGTTTTG
 CCCATATCTATTACCGTGTTCCTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAAACACCCAGCAAATTTGATTTTGATTATGGAATGAATTTGACAAAA
 GATTCCTTTGTGCCTGCTGAAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT
 TCTAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAAGCAGTGATGTATCCAGCCTTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG
 GGTATGCTTCGCATTTGATGGAATTTTTTGACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAATACCCCCGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTTGTGCGGGCCCTGAAGAGCAGGAGCTCAGTTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTTGAGAGTCGAGGCAGCGTTGGCAGTCTTGGGCCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGGCCGGAGGAAGAGCCATCGACGACCTGGTCGACTGGGATCCCC
 AACTGGCAGGCTGTGTATTCTTCGCTGTCCAGCTTCGACCAGGATTCAGAGGGCTGCGAG
 CCTTCTGAGGGGATGGGCTCGGAGAGGAGGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGT
 TATATGTGCAGATGGA**AACTG**ATGCCAACACTTCCTTTTGCCCTTTTGTTTCTGTGCAAC
 AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT
 TTGTGAGTGTCTGTGAGAATTACTTATTTCTTTTCTCTATTCTCATAGCACGTGTGTGATTG
 GTTCATGCATGTAGGTCTCTTAACAATGATGGTGGGCCTCTGGAGTCCAGGGGCTGGCCGGT
 GTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG
 TGGGTGT

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FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRVFKELKLLTLCSSIQIGPPEVALTTDEKSISVVLTAPEKWKRNPELPSVSMQ
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRIHVGKEKHPANLILYGNFED
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTIVIEYEDVRTTDICAGPEEQELSL
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLDPQAQEHDTSEEGPEEEPSTTLVDWD
PQTGRCLCIPSLSSFDQDSEGCEPSEGDGLGEEGLLSRLYEAPDRPPGENETYLMQFMEEW
GLYVQMEN
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG
TCTGCC**ATG**GGGGCTCGGGTTGAGGGGCTGGGGACGTCCTCTGCTGACTGTGGCCACCGCCCT
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG
TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA
GGCTTCCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT
CCGCACTGGCCTGGTGGTGTGGGCGCCACGTCCTGAGTACTGCGGAGCCCAACCAGCAGG
TGTTTGGCATCGATGCTCTACCACGCACCCCGACTACCACCCCATGACCCACGCCAACGAC
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCCTGGGCCCTGCAGTGGGGCTGCTGAGGCT
GCCAGGGAGAAGGGCCAGGCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT
TCGTGTCTGACTTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGTGGAC
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG
TGGGGACAGCCACAGAGGGGGCTTCTGCTCGGCCGACTCCGAGGGGCCCTGGTGTGCAGGA
ACCGGGCTCACGGCCTCGTTTCTTCTCGGGCCTCTGGTGCGGCGACCCCAAGACCCCGAC
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC
CCAGCCCGGCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCGCC**TGA**GCCACAACCT
TGCGGCATGCAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCCCACGGG
AAGCCTGATGTTACGGGTGGGGTGGGACGGGCAGCGGTGGGGCACACCCATTCCACATGCA
AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAAAAAAGAAA

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FIGURE 64

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGRF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGGACGCCTGACGCCCTGA
CGCCTGTCCCCGGGCCCGGCATGAGCCGCTACCTGCTGCCGCTGTGCGGCGTGGGCACGGTAG
CAGGCGCCGCCGTGCTGCTCAAGGACTATGTACCGGTGGGGCTTGCCCCAGCAAGGCCACC
ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT
GGAAGTGGCCAGGAGAGGAGGCAACATCATCTGGCCTGCCGAGACATGGAGAAGTGTGAGG
CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC
TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT
GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCACTGGACCACCGAGGACGGCT
TCGAGATGCAGTTTGGCGTTAACCACTGGGTCACTTTCTCTTGACAACTTGCTGCTGGAC
AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATGTTGCTGG
GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCTACT
GCCAGAGCAAGCTCGCCATCGTCTCTTACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT
GGTGTGACTGTCAACGCCCTGCACCCGGCGTGCCAGGACAGAGCTGGGCAGACACACGGG
CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
GCCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTT
TCCGGAAGTACTTCGATGGACTCAAACAGAAGCCCCGGCCCCCGAGGCTGAGGATGAGGA
GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA
GGGAGCAGCCCCCTCCCCAGATTAACCCTCTGGAGCAGATTTGAAAGCCAGGATGGCGCCTCCAG
ACCGAGGACAGCTGTCCGCATGCCCGCAGCTTCTTGGCACTACCTGAGCCGGGAGACCCAG
GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGGACTGGC
CTGCAGGTGAGCACTGCCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG
AGGGGCCATCTGATGCTTCCCTGGGAATCTAACTGGGAATGGCCGAGGAGGAAGGGGCTC
TGTGCACTTGCAGGCCACGTGAGGAGGCCAGCGGTGCCTGTGCGGGAGGGTTCCAAGGTGC
TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCTGTGGGACCT
TGTGCATGCATGGTCTCTCTGAGCCTTGTTTCTTACGACGTGAGATGCTCAGAATAACTG
CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGGG
GGTGTGTTGCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
GAGTTCAAGGCTCTGCACGGCATGGAGTGGGAACCCACCAGCTGCTGCTACAGGACCTGGGA
TTGCCTGGGACTCCACCTTCTATCAATTCTCATGGTAGTCCAACTGCAGACTCTCAAAC
TTGCTCATT

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FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNNARHLDLASLKSIREFAAKIIIEEERVVDILINN
AGVMRCPHWTEDGFEMQFGVNHLLGHFLLTNLLDLKLKASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSVREQPLPR

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTTCGCGAGCGCTGGC**ATGT**GGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTCGCGGCTCGGGGCGACACGTTCTCGGCGTGAC
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTACTTTCTTTGCGAT
 GAGGATTCAACAACCCCTGTGGCTAACCCTCTGCTTGCATTTACTCTCATCAAACGCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCAACGGCTCTTTCTCTCA
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTCACTCTCTCCGAGGATCTTACGGAGAGTGAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCGAGGAA
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAATATGAAAGGCTCTTGGCAGAGAGCCCAACCAGCTGGTAGC
 TGAGGCTGTCACTCAGAGGCCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC
 TATGTCAGACCCCTGGGTTCACAGCCCACTCTTACCAGATCCCTAGCCTCTACTGTTCCCTAT
 GAGACCAATTCCAACGCCCTACCTGCTGCTCCAGCCCATCCGGAAGGAGGTATCCACCTGGA
 GCCCTACATTGCTCTTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCAGTGGTGGCATCAGGGGAGAGCAAGATTACAAGTGGAG
 TACCGCATCAGAAAAAGTGGCTGGCTGAAGGACACTGTTGACCCAAAACCTGGTGACCCCTCAA
 CCACGCCATTGCTGGCTCACAGGCCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCACCAAGC
 AGCCCCCTCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTTCACTATGCCAACCTCAGCTGCGTGTGGTTAGGA
 ATGCAGCACTGTTTTGTGGAACTTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCTGCTGCTGGTGGGAGATAAGTGGGTGGCCAACAAGTGGATACATGAGTATGG
 ACAGGAATTCCGCAAGCCCTCGAGCTCCAGCCCTGAAGACT**TGA**ACTGTTGGCAGAGAGAAGC
 TGGTGGAGTCCCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCCTGGAAGAAGGCCTTGTCAGCTTTGTCTGTGCTCGCAATCAGAGGC
 AAGGGAGAGGTTGTTACCAGGGGCACTGAGAATGTACATTTGATCTGCCCGACCCACGGAA
 CTCAGAGTAGGATGCACAGTACAAGGAGGGGGGAGTGGAGGCCTGAGAGGGGAAGTTTCTGG
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTTCGATCAGTGGGTC
 TTTTGGCACTTTGAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAAGGAG
 GGGCTAGCCTGACTCCCAAGACTTTAAGACTTTCTCCCACTGCCTTCTGCTGCAGCCCAAG
 CAGGGAGTGTCCCCCTCCCAGAAGCATATCCCAGATGAGTGGTACATTATATAAGGATTTTT
 TTTAAGTTGAAAACAACCTTCTTTTCTTTTGTATGATGGTTTTTAAACACAGTCATTA
 ATGTTTTATAATCAAAA

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FIGURE 68

MGPGARLAALLAVLALGTGDPERAAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHVSLEASENIRALKDGYEKVE
 QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTSAITDLYSPKRLFSLTGDDCFQ
 VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGWKTEDASLEDALDHLAFAYFRAGNVSCALS
 LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHLQTRDTYEGLCQTLGS
 QPTLYQIPSLYCSYETNSNAYLLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
 RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLLSVEAGGATAFIYANLSVPVVRNAALFWW
 NLHRSGEGSDTLHAGCPVLVGDKWVANKWIEHYGQEFRRPCSSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTAAGTTCTGCTCCATCTCAGGAGGCCCTGCTCCACCCCTAG
GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGAGCCCCGTAACCCGCGCGGGGAG
CGCCAGGATGCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
TGGCTCAAGTTTCTACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCT
GTCTGTGGGCATCTATGCAGAGTTGAGCGGCAGAAATATAAAACCCCTTGAAAGTGCCTTCC
TGGCTCCAGCCATCATCCTCATCTCCTGGGCGTCTCATGTTTCATGGTCTCCTTCATGGT
GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT
CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCCTTGACCTTCCGGAACCAGACCATTG
ACTTCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA
AACATCATGGACTTTGTTCAGAAAAAGTTCAAGTCTGTGGCGGGGAGGACTACCGAGATTG
GAGCAAGAATCAGTACCACGACTGCACTGCCCCCTGGACCCCTGGCCCTGTGGGGTGCCCTACA
CCTGCTGCATCAGGAACACGACAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC
AAGGAGCGTTTCAGTGTGCAGGATGTCTACGTGCGGGGCTGCACCAACGCGGTGATCAT
CTGGTTTCATGGACAACCTACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT
TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC
TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGAGGCGGCAGGCACGGG
ATGCTGCTTGTGCTACCCCAATTAGGGGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
CTCAGTACTGACCAAAGCCAGGGCTGTGTGTGCCTGTGTGTAGGTCCCACGGCCTCTGCCTC
CCAGGGAGCAGAGCCTTGGGCTCCCCTAAGAGGCTTTCCCCGAGGAGCTCTGGAATCTGT
GCCACCTGGGGCTGGGGAACAAGGCCCTCCTTTCTCCAGGCCTGGGCTACAGGGAGGGA
GAGCTGAGGCTGTGCTCAGGGCCATTTCATCTCTGGCAGTGCCCTTGGCGGTGGTATTCAA
GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGAGGAGGGAAGG
GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTTGGC
CTCTTCTCAGCCTCCAGGTGCCTTGAGCCCTCTTGCAAGGGCGGCTGCTTCTTGGAGCTA
GTTTTTTTTTACGTGATTTTTGTAACATTCATTTTTTGTACAGATAACAGGAGTTTCTGAC
TAATCAAAGCTGATTTTCCCGCATGTCTTATCTTGGCCCTTCCCCAACAGTTTGTAA
TCAACAATAAAACATGTTTTGTTTTGTTTTTAAAAA

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FIGURE 70

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIILILLGVVMFMVSFIGVLASLRDNL YLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRG IENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIYVRGCTNAVIIWFM DNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCCAAGGTCTGGCATCCTGCACCTTGCTGCCCTCTGA
CACCTGGGAAGATGGCGGCCCGCTGGACCTTCACCCCTCTCTGTGGTTTGCTGGCAGCCACC
TTGATCCAAGCCACCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCCAAAAGTCATCAAAAGA
AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
TCAGTGCCATCGGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGGCAGCCTGGTGAACACC
GTCCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA
GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAAGCCACCATC
CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCCTCAGTGACTGTGCCACCAGCCA
TGGGAGCCTGCGCATCCAATGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC
AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACAGCTGTGTCCCGTG
ATCGAGGCTTCTTCAATGGCATGTATGCAGACCTCTGCAGCTGGTGAAGGTGCCCATTTT
CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT
AGCTCTACCTGGGGCCAAGTTGTTGGACTCACAGGGAAGGTGACCAAGTGGTTCAATAAC
TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCGTTCAGCCTCATCGTGAGTCA
GGACGTGGTGAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTATGGTCTGTGG
ACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG
GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCAGATT
TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTCCTCCCA
GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTTAC
ACCAAAGGTGACCAACTTATACTCAACTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
GAACTCTGGGATTGGCTGGTTCACACCTGATGTTCTGAAAAACATCATCACTGAGATCATC
ACTCCATCTGCTGCCGAACCAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCAATTGGTG
AAGGCCCTGGGATTGAGGCAGCTGAGTCCCTCACTGACCAAGGATGCCCTTGTGCTTACTCC
AGCCTCCTGTGTGAAACCCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT
CAATAAACACTTGCCTGTGAAAAA

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FIGURE 72

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILOQLPLLSAM
REKPAGGIPVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNLQCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDITQLYL
GAKLLDSQGKVTWKFNNASAASLTMPITLDNIPFSLIVSQDVVKAAVAVALSPPEEFMVLLDSVL
PESAHRLKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL
RPLFTLGIEASSEAQFYTKGDLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESSLTKDALVLT PASLWKPSSPVSQ
```

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAACATGGCGACGCGGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCCAAAGAAAGAAGGAGATGGTGTTATCTGA
 AAAGGTTAGTCAGCTGATGGAATTGGACTAACAAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCCGTCGCCTTGTGAAAGCCCCACCGAGAAATTACTCCGTTATCGTCATGTTTCACTGCT
 CTCCAACCTGCATAGACAGTGTGTCTGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACACAGGATATTTTTGCCATGGTGGGATTTG
 ATGAAGGCTCTGATGTATTTCAGATGCTAAACATGAATTCACTCCAACCTTTCATCAACTTT
 CCTGCAAAAGGGAACCCAAACGGGGTGATACATATGAGTTACAGGTGCGGGGTTTTTCAGC
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAAGCTGATGCAATATAGAGTGATTAGACCCC
 CAAATTATGCTGGTCCCCCTTATGTTGGGATTGCTTTTGGCTGTTATTGGTGGACTTGTGTAT
 CTTTGAAGAAGTAATATGGAATTTCTCTTTAATAAACTGGATGGGCTTTTGCAGCTTTGTG
 TTTTGTGCTTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTTGTA
 GCTGAAACACACATTGTTCTTCTGTTTAAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG
 TGAAGCTGCTACCTCTGACATGGATATGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG
 GACTTGTTGTATTATTCTTCAGTTGGATGCTCTCTATTTTATAGATCTAAATATCATGGCTAC
 CCATACAGCTTTCTGATGAGTTAAAAAGGTCCTCAGAGATATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTGTTTGAAGAAGAATGCAACTTGTATATTTTGTATTAC
 CTCTTTTTTTTCAAGTGATTTAAATAGTTAATCATTAAACCAAAGAAGATGTGTAGTGCCTT
 ACAAGCAATCCTCTGTCAAATCTGAGGTATTTGAAAATAATTATCCTCTTAACCTTCTCTT
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTATAAAAATTTGAAAA
 CTACTACTTTGTTTTAGTTAGAACAAAGCTCAAAACTACTTTAGTTAACTTGGTCATCTGAT
 TTTATATTCGCTTTATCCAAAGATGGGGAAGTAAGTCTCGACCAGGTGTTCCACATATGCC
 GTTACAGATAAATACATTAGGAATTCATTCTTAGCTTCTCTCATCTTTGTGTGGATGTGTAT
 ACTTTACGCATCTTTCTTTTGTAGTAGAGAAATTATGTGTGTCATGTGGTCTTCTGAAAATG
 GAACACCATTCTTCAGAGCACACGCTAGCCCTCAGCAAGACAGTTGTTTCTCTCTCTCTCT
 GCATATTTCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTAACTACCTTGTATTTAGAAA
 GATTTAGATTTCATTCATCTCTCTTAGTTTTCTTTTAAAGGTGACCCATCTGTGATAAAAATA
 TAGCTTAGTGCTAAAATCAGTGAACCTTATACATGGCCTAAAAATGTTTCTACAAAATTAGAGT
 TTGTCATCTATTCCATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGCGCAGCTGACTTACGCTGTAACTCTCAGCACTTTGGGAGGCCAGGCGAGCTGATCAC
 GAGGTGAGGAGTTTCGAGACCATCTCTGGCCAACATGGTGAACCCCGCTCTACTAAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCAGCTACACAGGAGGCTGAGGCAC
 GAGATCACTTGAACCTCAGGAGATGGAGGTTTCACTGAGCCGAGATCACGCCACTGCCTCC
 AGCCTGGCAACAGAGCGGAGACTCCATCTCAAAAAAAAAAAAAA

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FIGURE 74

MAARWRFWCVSTMVVALLIVCDVPSASAQRKKEMVLSEKVSQMLEWTNKRFPVIRMNGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG
SDVFQMLNMNSAPTFFINFPAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAACTGCAAGCTTTGGGAGTTGTTGCTGTCCCTGCCCTGCTCTGCTAGGGAGA
 GAAGCCAGAGGGAGGCGGCTGGCCCGGGCGGAGGCTCTCAGAACCGCTACCGGCGCATGCTA
 CTGCTGTGGGTGTCGGTGGTCGCAGCCTTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
 GCAGAGGCGGAGAGCAGCCAAAGCGCCCAATGTGGTGCTGGTCTGAGCGACTCCTTCGATG
 GAAGGTTAAACATTTTCATCCAGGAAGTCAGGTAGTGAACCTTCCTTTTATCAACTTTATGAAG
 ACAGTGGGACTTCCTTTCTGGAATGCCTACACAACTCTCCAATTTGTTGCCCATCAGCGC
 AGCAATGTGGAGTGGCCCTCTTCACTCACTTAACAGAATCTTGAATAATTTTAAAGGGTCTAG
 ATCCAAATTATACAACATGGATGGATGTCATGGAGAGGCGATGGCTACCGAACACAGAAATTT
 GGGAACTGGACTATACTTCAGGACATCACTCCATTAGTAATCGTGTTGGAAGCGTGGACAAG
 AGATGTTGCTTTCTTACTCAGACAAGAAGGCGAGGCCCATGGTTAATCTTATCCGTAAACAGGA
 CTTAAGTCAGAGTGATGGAAGGGATTGGCAGAATACAGACAAGCAGTAACCTGGTTAAGA
 AAGGAAGCAATTAATTACACTGAACCATTTGTTATTTTACTTGGGATTAAATTTACCACACC
 TTACCCCTTCAACATCTTCTGGAGAAAAATTTTGGATCTTCAACATTTTACACATCTCTTTATT
 GGCTTGAAAAAGTGCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTTTGTGAGAAATG
 CACCCTGTAGATTATTACTCTTCTTATACAAAAAACTGCACTGGAAGATTTACAAAAAAGA
 AATTAAGAATATTAGACATTTTATTATGCTATGTGTCTGAGACAGATGCCATGCTTGGTG
 AAATTTATTTTGGCCCTTCATCAATTAGATCTTCTTCAGAAAACTATTGTCATATACTCCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTTATAAAAAGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTTGATGATGGGACCAGGAATTAAGCCGCGCCTACAAGTATCAAAATG
 TGGTTTCTCTTGTGGATATTTACCCTACCATGCTTGATATTGCTGGAATTCCTCTGCCTCAG
 AACCTGAGTGGATACTCTTTGTTGCCGTTATCATCAGAAACATTTAAGAATGAACATAAAGT
 CAAAAACCTGCAATCCACCCTGGATTCTGAGTGAATTCATGGATGTAATGTGAATGCCCTCCA
 CCTACATGCTTCGAACTAACCACTGGAATATATAGCCTATTCCGATGGTGCATCAATATTG
 CCTCAACTCTTTGATCTTTTCCCGGATCCAGATGAATTAACAAATGTTGCTGTAATAATTTCC
 AGAAATTACTTATTCTTTGGATCAGAAGCTTCATTCCATTATAAACTACCCTAAAGTTTCTG
 CTTCTGCTCCACGATATAATAAAGAGCAGTTTATCAAGTGGAAACAAAGTATAGGACAGAAT
 TATTCAAACGTTATAGCAAACTCTTAGGTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTA
 TGAAAAATGCAATTGATCAGTGGCTTAAAACCCATATGAATCCAAGAGCAGTTTGAACAAAAA
 GTTTAAAAATAGTGTTCTAGAGATACATATAAATATATTACAAGATCATAATTATGTATTTT
 AAATGAACAGTTTTTAATAATTACCAAGTTTTGGCCGGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTTGGGAGGCTGAGGAAAGCAGATCACAAAGTCAAGAGATTGAGACCATCCTGGC
 CAACATGGTGAACCCCTGTCTCTACTAAAAATACAAAAATTAGCTGGGCGCGGTGGTGCACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTTGAACCCGGGAGGCAGCAG
 TTGCAGTGAGCTGAGATTGGCCCACTGTACTCCAGCCTGGCAACAGGTGAGACTGTGTCCG
 AAAAAAATAAAAAATAAATAATAATAATTACCAATTTTTCATTATTTTGTAAAGATGTAGTG
 TATTTTAAAGATAAAATGCCAATGATTATAAAATACATATTTTCAAAATGGTTATTTATTTA
 GGCTTTGTACAATTTCTAACAAATTTAGTGGAAAGTATCAAAAGGATTGAAGCAAAATACGTA
 ACAGTTATGTTCCCTTTAAATAATAGAGAATATAAAATATTGTAAATAATATGTATCATAAAAAT
 AGTTGTATGTGACATTTGATGGTGAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

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FIGURE 76

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRITFHGPSQVVKLPIFINF
MKTRGTSFLNAYTNSPICCPSTRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPVNLIRNRTKVRVMERDQNTDKAVNW
LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSTYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGETIILALHQLDLLQKTIVIIY
SSDHGELAMEHRQFYKMSMYEASAHVPLMMGPGIKAGLQVSNVSVLVDIYPTMLDIAGIPL
PQNLSGYSLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTVAVKFFETIYSLDQKLHSIINYPKVSASVHQYNKEQFIKWQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIQWLKTHMNPRAV
```

Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416, 498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

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FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT
GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGGTGCCAGCATTGTGACAG
CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
TGTGACATCTATAGCACCTTCTGGGCTGCCCGTGACATCCAGGCTGCCAGGCCATGAT
GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA
CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC
ATCCTTGAGGGCCTCCTGGGATTCATTCTCTGTGCTGGAATCTTCATGGGATCCTACGGGA
CTTCTACTCACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG
GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC
CAGAGAAATCGCTCCAACTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC
TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT
ATGTG**TGA**AGAACCAGGGGCCAGAGCTGGGGGTGGCTGGGTCTGTGAAAAACAGTGGACAG
CACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGG
ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAACAGCATG
CAGGTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC
CCCTGCCCTAAGTCCCCAACCTCAACTTGAAACCCCATTCCTTAAGCCAGGACTCAGAGG
ATCCCTTTGGCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG
ACTGACCCCTCTGTGATCAAAGACCCCTCTCTCTGGCTGAGGTGGCTCTTAGCTCATTTGCTGG
GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
TCCAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC
AGACTAATTTGTGATGAAGTAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVG YILG LLLG LGLVAMLLPSWKTSSYVGASIVTAVGFSGKLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGLLGFIPVAWNHLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCS
SQNRNSNYDAYQAQPLATRSSPRGQPPKVKSEFN SYSLTGIV
```

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

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FIGURE 79

GCCTGCTGCTGTCCCATCAGCTGCTCTGAAGCTCCATGGTGCCCAGAATCTTCGCTCCTGC
TTATGTGTCAGTCTGTCTCCTCCTCTTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCTTTGGCCTCACAAACGATTTTGTTG
TGAAGCTGAAGGTTCAAGGTGTGAATCCCAGTGCCACTCATCTCCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTTCCCTTGAGAAGACATAGAAAGAAAATCAACTTTCACCTAAGGCATC
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAAATAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

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FIGURE 80

MVPRI FAPAYVSVCLLLCPREVIAPAGSEPWLCQPAPRCGDKIYNPLEQCCYND AIVSLSE
TRQCGPPCTFWPCFELCCLDSFGLTND FVVKLVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

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FIGURE 81

CTCCACTGCAACCACCCAGAGCC**ATGG**GCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAAGTGCAG
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCT**TAA**TGGAACATCAGGGGAA
CGATGACTCCTGGATTCTCCTTCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACACTCAACTGCCCACTTCATT
CTGTGACCTGTCTGAGGCCACCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCTTCACCTT
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTTATGTACTTTATAAATGAAAA

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FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCDSARTSDDRLCRSVS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCCGCAGCGCTCACTCGCTCGCACTCAG
 TC GCGGGAGGCTTCCCCGCGCCGGCCGCGTCCCGCCCGCTCCCGGCACAGAAAGTTCCTCT
 GCGCGTCCGACGGCGACATGGGCGTCCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA
 TCCCTGCTCTTCGCTCTCTTCTCGGTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGGTGCG
 CACGCCGTATTCCCTGTATGTCTGTCCCGAGGGGCAGAACGTACCCCTCACCTGCAGGCTCT
 TGGGCCCTGTGGACAAAGGGCAGCATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG
 GCGAGGTGCAGACCTGCTCAGAGCGCGGCCCATCGCAACCTCAGTTCCAGGACCTTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGCAACCTGACCCCTGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCCTCGGAGCACAGGGT
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAGAAAGATGCACCATCCAACCTGTGTGGTGT
 ACCATCCTCTCTCCAGGATAGTGAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCTGGTCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCGCTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAGAAC
 CCGGCTTTGAAGCCTCACACCTGCCAGGGGATACCCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGGCGCATCTGCTTTCGGAGCCCAGCAC
 CCCCCTGTCTCTCCAGGCCCGGAGACGTCTTCTCCCATCCCTGGACCCTGTCCCTGACT
 CTCCAACCTTTGAGGTCACTTAGCCCAGCTGGGGACAGTGGGCTGTTGTGGTGGGTCTGG
 GGCAGGTGCATTGAGCCAGGGCTGGCTCTGTGAGTGGCTCCTTGGCTCGGCCCTGGTTT
 CCTCCCTCTGCTCTGGGCTCAGATACTGTGACATCCCAGAAGCCAGCCCCCAACCCCTC
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGGTGTGAG
 ATTCTCCCTAGAGACCTGAAATTCACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA
 GCATCAGTGGGACAAGATGGACACTGGGCCACCTCCAGGCACCAGACAGGGCAGCGTG
 GAGAGACTTCTCCCCGTGGCCGCCCTTGGCTCCCCCGTTTGCCCGAGGCTGCTCTTCTGTC
 AGACTTCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCTGCCCACTGGCCATCGCC
 ACCTTCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC
 ATATTGGGGCATGGTGGCTCCGTGAGCAAATGGTGTCTTGGCAATCTGAGGCCAGGACAG
 ATGTGCCCCACCCACTGGAGATGGTGTCTGAGGGAGGTGGTGGGGCTTCTGGGAAGGTGA
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCCATCCCCTACTCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAATACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

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FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897

><subunit 1 of 1, 311 aa, 1 stop

><MW: 33908, pI: 6.87, NX(S/T): 6

MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFAQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ
DSENITAAALATGACIVGILCLPLILLVYKQRQAASNRRQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCCTCCT
 TTCCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCCACCTTAGACCTCCCTTCTCTGCCCTCC
 TTTCTTGCCACCGCTGCTTCTCGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCTTTTCGTCTCCCTTCTCTCCCGA
 CTCCGCTCCCGACCGAGCGCCCTGACCCTGGGGAAGGATGGTTCCCGAGGTGAGGGTCTCTC
 TCCTCCTTGCTGGGACTCGCGCTGCTCTGGTTCGCCCTGGACTCCACGCTCGAGCCCGCCC
 AGACATGTCTGCTTTTTCCATGGGAAGAGATACTCCCCGGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGGCCCAACAAAGTCTTGCC
 AGCACACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCTCC
 CGCCTGCCCAACCAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCCTCAC
 AACCTGCCCCGAACCAGGCTGCCCAGACCCCTCCCACTGCCAGACTCTGCTGCCAAGCCT
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG
 AGACATCCTCAGATCCATGTTCCAGTGATGCTGGGAGAAAGAGAGGCCCGGGCACCCAGC
 CCCCCTGCGCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGTCTCTGAAGGAGAAACATAAGAAAGCCTGTGTGCATGGCGGG
 AAGACGTACTCCCACGGGGAGGTGTGGCACCCGGCCTTCCGTGCCTTCGGCCCTTGCCTTG
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCCACCGAGT
 ACCCCTGCGCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTTGCCAGAGGACAAA
 GCAGACCCTGGCCACAGTSAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGGTCTCT
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGTCGCTTTGCCCTGGAACACGAGG
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA
 AAGTCAGGAAGCAAGACTTCCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCCAC
 GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTACAGGCCAGTCCAGA
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT
 ATTATATATTAATAAATAAGAAGTGCATTACCCCTCAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 86

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSLLGLALLWFPLDSHARARPD MFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCFPVHCPQPVTEPQQCCPKCEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDDED
SVQSLHGVRHPQDPCSSDAGRKRGPPTAPTGLSAPLSFIPRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPTTEYPCRHPKAVAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLVKLV
KDEETEAQRGEVPGFRPHSQNLPLDSQESQEARLPERGTALPTARWPPRRSLERLPSDPDG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

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FIGURE 88

MDSLRLKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLLA
TLQEAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

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FIGURE 90

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46038, pI: 6.50, NX(S/T): 2

MGPSTPLLLILFLLSWSGPLQGQHHLVEYMERRLAALAEERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDGTYISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL
RDFTLAMAARKASRVVPFPWVGTTGQLVYGGFLYFARRPPGRPGGGGEMENTLQLIKFHLAN
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCCLAKLDPQTLDEQ
QWDTPCPRENAEAAAFVICGTLVYVYNTRPASRARIQCSFDASGTLTPERAALPYFPFRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTGCTCGATGGAGTAGACTCTCAGAACAGCGAGTTTGCCCTCCGCTCAGCGAG
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTTCTCTAATCCAT
 CCGTCACCTCTCCTGTCTATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**
 CTCTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGCAGCATTCTCCTGTTTCTGTCTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTTCAGGGGCCAGTTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCATTATGTCAGATGCCACAGTATCAAGGCAGG
 ACAAACTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAAAACATTAC
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTTCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCTAGTCTCGGGCTGGTTCCCCCGGCCACAGCGAAGTG
 GAAAGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGGAGCATATCTCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG
 GCATTGTTGGACTGAAGATTTTCTTCTCCAATTCAGTGGAATAACAGGCGGAAGTGGAC
 TGGAGAAGAAGACGGACAGGCAGAAATTGAGAGACGCCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAACGTGAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTG
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCGAGGACCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAGTG
 TGGGACCATCTCCTTCTTCAACATAAATGACCACTCCCTTATTATACCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTCTATAATGAGCAAAATGGAAGTCCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCCTCTTGCCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCTCTCTCACAGGCAACCAGCCCTTCTCCCCAGGG
 GTGAAAT**GTAGG**ATGAATCACATCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCA
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAAGTGTCTATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTT
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTTCATTATATTACACTTTCAGTA
 AAAAAA

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FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAAFSCFLSPKTNAEAMEVRFFRGQFSS
 VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRIS SQSY YQK
 AIWELQVSALG SVPLISITGYVDRDIQLLCQSSGWFFRPTAKWKGPQGQDLSTD SRTNRDMH
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
 FGIVGLKIFFSKFQWKIQAE LDWRRKHGQAE LR D ARKHAVEVTLD PETAH PKLCVSDLKTVT
 HRKAPQEVPHSEKRFTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS
 PDHGYWVLRNLNGEHL YFTLNPRFISVFFRT PPTKIGVFLDYECGTISFFNINDQSLIYTLTC
 RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASQWRASAI PETSNSSESSQATTFPLP
 R GEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCGCCCGGTGGCGGTGGCGGCGCGGTTGCGGAGGCTTCCTTGGTGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC
CATGAGGAGCCTGCCGAGCCTGGCGGCGCTCGCCCTGTTGTGCTGCGCCGCGCGCGCGCGCGG
 CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTACCGGTGGCGGCGGGGCGCGGGGCAAGTG
 GACGCGTCGCGCGGCGCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTTAGGCGACGCGC
 TCCACGCGCCAGGCCCGAGGACC GGCGCCCGCGCGCCACCTCCACCGACCCCTGGCTG
 CGACTTCTCCAGCCAGTCCCGGAGACCACCCCTCTTTGGGCGACTGCTGGACCCCTCTTCC
 ACCACCTTTTCAGGCGCGCTCGGCCCCCTCGCCGAGCACCCCTCCGGCGCGGAACGCACCTTC
 GACCACCTCTCAGGCGCCGACGACCCGCGCGGACCCCTTTTCGACGACCACTGGCCCGG
 CGCCGACCAACCCCTGTAGCGACCAACCTACCGGCGGCCACGACTCCCGGACCCGACCCCGC
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCTCTCTCCAGAGTATGTATGTAAGTCTGTGGTTGGAAGCCTGAATGTGAATCGCT
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACTGTGAACCT
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTGAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAAGTGAAGTTTATT
 TTATTTTAGCTAAGGAAAAAAGGCTGCTACTCTCAAGGACCACTAGGTTTAAACAAAG
 GAGGATGAGGGTCATAGATTTACAAAATATTTATATACCTTTTATTCTCTTACTTTATATGT
 TATATTTAATGTCAGGATTTAAAAACATCTAATTTACTGATTTAGTTCTTCAAAGCACTAG
 AGTCGCCAATTTTTCTCTGGGATAATTTCTGTAAATTTTCATGGGAAAAAATTATTGAAGAAT
 AAATCGCTTTCTGGAAGGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAGTGTCTT
 ATGTTTATTAATATACCATTTGAGTTTGGAGAAATTTGTTGTTTGGTTTATTTTTCTCTCTA
 ATCAAAATCTACATTTGTTTCTTTGGACATCTAAAGCTTAACTGGGGTACCCTAATTTA
 TTTAACTAGTGGTAAGTAGACTGGTTTTACTCTATTTACAGTACATTTTGGAGACCAAAAG
 TAGATTAAGCAGGAATTATCTTTAACTATTATGTTATTTGGAGGTAAATTAATCTAGTGGA
 ATAATGTACTGTTATCTAAGCATTTGCCTTGTACTGCACTGAAAGTAATTATTCTTTGACCT
 TATGTGAGGCACTTGGCTTTTTGTGGACCCCAAGTCAAAAACCTGAAGAGACAGTATTAAT
 AATGAAAAAATAATGACAGGTTATACTCAGTGTAACCTGGGTATAACCAAGATCTGCTGC
 CACTTACGAGCTGTGTTCCCTTGGGCAAGTAATTTCCCTTCACTGAGCTTGTCTTCTCAAG
 GTTGTGTGAAGATTAAATGAGTTGATATATATAAATGCCTAGCACATGTCACTCAATAAA
 TTCTGGTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTTATACCTTTAGCACTAAATATTTAAATGCTTTA
 TAAATGATATTATCTGTTATGGAATATTGTATCATATTTAGTTTATTAAAAATGTAGAAG
 AGGCTGGGCGCGGTGGCTCACGCGCTGTAATCTAGCACTTTGGGAGGCCAAGCGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGCTCTACTAAA
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACCTGTAGTCCCAGCTACTCGGGAGGCT
 GAGGCAGGAGAATCGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCCACT
 GCATCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAA

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FIGURE 94

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGGGLALLCCAAAAA VASAASAGNVTGGGGAAGQVDASPGPGLRGEP SHPFPRATA
PTAQAPRTGPFPRATVHRPLAATSPAQSPETTPLWATAGPSSTTFQAPLGPSTTPPAAERTS
TTSQAPTRPAPTTLSTTTGPATTPVATTVPAPTTPTPTDLPSSSNSSVLPTPPATEAPS
SPPPEYVCNCSSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR

Important features of the protein:**Signal peptide:**

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

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FIGURE 95

TGCGGCGCAGTG TAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG
TCTCGGTGCCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGGTGGTGGTGACCCTCACTCCAGAAAACAACCTGCGGACGCTGTCCTCTC
AGCACGGGCTGGGAGGGTGTGACCAGAGTGT CATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTTGAGAATCCCTCAATAGGCGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTACCAAGTGGAGCAGGAGC
CTGGGCTTCCTGTACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA
GTGTCCACCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT
CACAGCA

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FIGURE 96

MGGLLLAAFLALVSVPRQAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRTLSSQHGLGGCDQSVMDLIKRN SGWVFENPSIGVLELWVLATNFRDYAIIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

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FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCAGACATGCTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGACAGGAAGGCCTGTGTTCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT
 GGCTGGATTACCTTGGCCAGTAGTTCATGGCTACTGGTTCGGGAAGGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC
 GATTCCACCTCCTTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCCAACATCCTCATCCAG
 GCACCTTGGAGTCCGGCTGCCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCTGTGAGCAG
 GGGACACCCCTATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCTTAC
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCTGTGCCCC
 TCACAGCCCTCAAACCCGGGGGTGCTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA
 ATTCACCTGCAGAGCTCAGAACCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGGAGCTGGAGCCACAGCCCTG
 GTCTTCTGTCTTCTGCGTCTATCTTCGTTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAAACGCTGTGAGGGGTTAGCCT
 CTCAGGGGCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCCAGACCAGCCTCCCCCAGCT
 TCTGCCCCGCTCCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGTCAAGATCC
 ACAGATGAAGAACTGCAGAGACTCACCCCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTTATTTTTTTAACTAAAAGACAGACAAATTCCTA

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FIGURE 98

MLLLLLPLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSPWACEQGTTPPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMTVFQGDG
TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLVSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS
CRKKSARPAAGVGDTGIEDANAVRGSSASQGPLTEPWAEDSFPDQPPPASARSSVGEGELQYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

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FIGURE 99

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAGATGAAAGACCCTGTTCTCTG
GGTGTACAGCTCGGCCTGGCCGCTGCCCTGTCCTTCACCCCTGGAGGAGGAGGATATCACAGG
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCCGGAGGACAGGAGGCCAGGA
AGGTGTCCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC
ATGAGGGAGGATCGGTGCATCCAGAAGAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCAGGAGGGACCACT
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCTGCTCCACATGGGAAAGCTTGTGGGT
AGGAATTCTGATACCAACCGGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG
ACTCTCGGAGGAGGACATTTTCACGCCCCTGCAGACGGGAAGCTGCGTTCCCGAACACTAGG
CAGCCCCCGGTCTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT
GGACCTACCCTCCAGCCATGACCCTTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT
TTTCCCCCAA

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FIGURE 100

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404

<subunit 1 of 1, 170 aa, 1 stop

<MW: 19457, pI: 9.10, NX(S/T): 0

MKTLFLGVTGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVS PVKV TALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCTCTGGCAACAGGGCTTGAGGGGAGAGACCAGGATCATCAAGGGGTTTCGAG
 TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTTCGAGAAGACGCGGCTACTCTGTGG
 GCGCAGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCGCTACA
 TAGTTACCTGGGGCAGCACAACTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC
 AGCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAAACATCACCATCATTTGAGCACCA
 GAAGTGTGAGAACGCCTACCCCGGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC
 GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA
 CCCACCACAGCCCATCACCTCCATTTCCACTTGGTGTTTGGTTCCTGTTCACTCTGTTAAT
 AAGAAACCCTAAGCCAAGACCCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGGTTCGAAATCAGTGAGACCTGGATTCAAATCTGCCTT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTTGCTAAATGAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 102

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405

<subunit 1 of 1, 250 aa, 1 stop

<MW: 27466, pI: 8.87, NX(S/T): 4

MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCSLISGWGSTSSPQLRLPHTLRANITIIIEHQKCENAYPGNITDTM
VCASVQEGGKDCQGDSSGGLVCNQSLQGIISWQDPCAITRKPGVYTRVKYVDWIQETMKNN

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

GAGCAGTGTCTGCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTCAGATTCATTGTTT
TCTTTTATCTGTGGGGCCTTTTTACTGCTCAGAGACAAAAGAAAGAGGAGACCCGAAGAA
GTGAAAATAGAAGTTTTGCATCGTCCAGAAAACCTGCTCTAAGACAAGCAAGAAGGGAGACCT
ACTAAATGCCCATATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCTACTGCAGCCGGA
CACAAAATGAAGGCCACCCCAAATGGTTTGTCTTGGTGTGGGCAAGTCATAAAAGGCCTA
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCTTCATT
TGCATACGGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAAGA
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT
GAACTATAGCATATTTGTATTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA
AAACAAAGTCACTTTTCTCCAAGTTGTATTTGCTATTTTTCCCTATGAGAAGATATTTTGA
TCTCCCCAATACATTGATTTTGGTATAATAAATGTGAGGCTGTTTTGCAAACCTAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDDHGDGFI SPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

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FIGURE 105

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTCTGCTGAGCCTCTTTGGAGCT
GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAGGAGTTTGAGACCAGCCTGGCCAACATAGTGA AAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGGCGTGGTGGTGCATGCCGTGCAATCCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTTCTTGTTTCATTTTCGCGACTGCCCTCTCAGTGTTTCTGGGATCCCCCTCCCAATAA
AGTACTTATATTCTC

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FIGURE 106

MQGPLLLLPGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHTCTCNHGYTSGSGQKLFTFPL
ETCNARHGG SRL

Signal peptide:
amino acids 1-18

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FIGURE 107

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGGCAC
AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACCATGG
GGCTCAGCATCTTTTGTCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACACCGAAGATT
TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC
CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA
GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCGAG
CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA
CGAGCACGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACAGCAGCGTTCAAC
CCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGGC
ATCACCAACCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT
CTCCCATGCCACCTGCCATGGTGTGTATCCCGGAGAATCACGAGCAACATGGTGTGTGCAG
GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA
GTCCTTCAAGGTCTGGTGTCTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG
AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAACTGAC
CTGTTTCTCCACCTCCACCCCCACCCCTTAACCTTGGGTACCCCTCTGGCCCTCAGAGCACC
AATATCTCCTCCATCACTTCCCTAGCTCCACTCTTGTGGCCTGGGAACTTCTTGGAACCTT
TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGTCTGGA
ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

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FIGURE 108

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH
 CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLRLPVRVTSSV
 QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
 AGGVPGQDACQGDSGGPLVCGGVLLQGLVSWGSGVGPCGQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

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FIGURE 109

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCTCGC
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATGT**CGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGGCGTTTCGGCTTGCTCAAAGCCCGCAGGAGAGGAGGCTGGCC
 GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCTTCCAGAAAA
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAAATGAAGGCGAGATTGACC
 TGATGTCCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGGTCAGTGACACTATATCCTACCGAGACTTTGTGAA
 CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTGAAGGAAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCTCATTGTTTGGTTCATTGAGGGTTTGTGTTGTTT
 TCATCAATGTCCTTTGTAAAGCACAAATATCTGCCTTAAAGGGGCTCTGGGTCGGGGAATCC
 TGAGCCTTGGGTCCCTCCCTCTCTTCTCCCTCCTTCCCGCTCCCTGTGCAGAAAGGCTG
 ATATCAAACCAAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTCCC
 CTCACTTGGAGGAACAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTTCGGGTTTCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTCGGGGCCCGCTGCCCAAGCTGATCCCACTCATTCCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGAGCTTGGCATTGGGAGCCCTTCAAGAAGG
 TACCAGAAGGAACCTCCAGTCTGTCTCTGCGCCACACCTGTGCAGGAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG
 GGGTTTGGGGGGAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGGAGAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTGTGCTGACCCCAATCTGCTTGAAAAA

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FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEGINREFLCDQKYSDEENLPEKLTAFKEKYMEDLN
NEGEIDLMSLKRMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKLV
MFEGKANESSPKPVGPPPERDIASLP

FIGURE 111A

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCTCCA
 GGAGCGGGGCCCTGCACACCA**ATG**GGCCCCGGGTGGGCAGGGGTCGGCGCGCCGTGCGCGCC
 CGCTTGGCGCTGGCTTGGCGCTGGCGAGCGTCTTGAGTGGGCTCCAGCCGTGCGCTGCC
 CACCAAGTGTACTGCTCCGCTGCCAGCGTGGACTGCCAGGGCTTGGCGCTCCGCGCGGTTT
 CTCGGGGCATCCCCCGAACGCTGAGCGCTTGACTTGCAGAAATATATACCAGGATC
 ACCAAGATGGACTTTCGTGGGCTCAAGAACCCTCCGAGTCTTGATCTGGGAACAACAGGT
 CAGCGTCATCGAGAGAGGCGCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCGCCTGAACA
 AGAATAAGTGAAGTCCTTCCAGAATTGCTTTTCCAGAGCAGCCCGAAGCTCACCAGACTA
 GATTTGAGTGA AACAGATCCAGGGGATCCCGAGGAAGGCGTTCCGCGGCATCCAGGATGT
 GAAGAACCCTGCAACTGGACAACAACACATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC
 TGCGCGATTGGAGATCCTTACCCTCAACAACAACAACATCAGTCGCATCTGTGTCACGAGC
 TTCAACCACATGCGGAAGATCCGAACCTGCGCCTCCACTCAACCACCTCTACTGCGACTG
 CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTACACTCT
 GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAAGAAGGAGTACGTG
 TGCCAGCGCCCCCATCGGAGCGCCCATCTTGCATGCCAATCCATCTCTGCTGCCCTTCGCC
 CTGACGTGCAGCAATAACATCGTGGACTGTGCAGGAAGGGCTTGATGGAGATTCTGCGCA
 ACTTGGCCGAGGGCATCGTCGAATACGCCCTAGAACAAGACTCCATCAAAGCCATCCCTGCA
 GGGCCTTCCAGCCAGTCAAGAAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TAGTCTCCAGATGCGCTTACAGGGCTGAAATCACTACATCGCTGGTCTGTATGGGAACA
 AGATCACCAGAGATTGCCAAGGGACTGTTTGTATGGGCTGGTGTCCCTACAGTCTCTCTCTC
 AATGCAACAAGATCAACCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAGCTGCAGACCATCAGCAAGGGGCTCTTCCGCCCTTCGAGT
 CCATCCAGACACTCCACTTAGCCCCAAAACCCATTTGTGTGCGACTGCCACTTGAAGTGGGT
 GCCGACTACCTCCAGGACAACCCCCATCGAGACAAGCGGGGCGGCTGCGAGCAGCGCCGCGC
 ACTCGCCACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTTCAGCGCAGTGTCTCATGGACCTCGTGTGCCCCGAGAAGTGTCCG
 TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGCAATCCCAAGCCACCTCCC
 TGAATATGTACCGACTCGGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAAGTTGCCAACCTGCGGAAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTTCGATGGAGACGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT
 GGAGACCGTGCAAGGGCGCGTGTTCCTGGCCTCAGTGGCCTCAAACCTTGATGCTGAGGA
 GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTTCGGTGAGACTGCTG
 TCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTACCACCGCTTGTCTCCCT
 GTCCACCATAAACCTCTGTGCCAACCCCTTCAACTGCAACTGCCACTGGCCTGGCTCGGCA
 AGTGGTTGAGGAAGAGGCGGATCGTCAGTGGGAACCCTAGGTGCCAGAAGCCATTTTTCCTC
 AAGGAGATTCCCATCCAGATGTGCCATCCAGGACTTCACTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCGCGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT
 GCAGCAACAAGGGGCTCCGCGCCCTCCCGAGAGGCATGCCCAAGGATGTGACCCGAGCTGTAC
 CTGGAAGGAAACCACTTAACAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACTGACGCT
 TATTGACTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCAGTAACATGTCTC
 ACCTCTCCACTCTGATCTGAGCTACAACCGGCTGAGGTGCATCCCGCTCCAGCGCTTCAAC
 GGGCTGGGTCCTTGGAGTGTAACTAACCTCCATGGCAATGACATTTCCAGCGTCTCTGAAGG
 CTCCTTCAACGACCTCACATCTCTTCCATCTGGCGCTGGGAAGCAACCACTCACTGTG
 ACTGCACTTCTCGTGGCTGTGCGAGTGGTGAAGCGGGGTACAAGGAGCCTGGCATCGCC
 CGCTGCAGTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCACCGCTT
 CCAGTGCAAGGGCCAGTGGACATCAACTTGTGGCCAAATGCAATGCCTGCCTCTCCAGCC
 CGTGCAAGAATAACGGACATGCACCCAGGACCTTGTGGAGCTGTACCGCTGTGCTGCCCTGCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTACAGTGCTCCTGCCCTC
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACAAATGCCACCTGGCGTGGACGGGATCAACAACCTACGTGTGTAATCTGTCCGCCTAACTACAC
 AGGTGAGCTATGCGACGAGGTGATTGACCACTGTGTGCCCTGAGCTGAACCTCTGTGAGCATG
 AGGCCAAGTGCAATCCCCCTGGACAAAGGATTGAGCTGCGAGTGTGTCCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTG
 AACACCCCCACCCATGGTCCCTACTGCAGACCAAGCCCATGCGACCAAGTACGATGCCAGAAC
 GGGGCCAGTGCAATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAAGGCTTCGCCGG
 CCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAGACTCCTACGTGGAAGTGG
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACAAC
 GGCATCCTTCTCTACAAGGAGACAATGACCCCCTGGCACTGGAGCTGTACCAGGGCCACGT
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCAAGTGTACAGTGTGGAGACAGTGA
 ATGATGGGCAGTTTACAGTGTGGAGCTGGTGACGCTAAACCAGACCTGAACCTAGTAGTG
 GACAAAGGAATCCAAAGAGCTTGGGAAGCTCCAGAAGCAGCCAGTGTGGCATCAACAG
 CCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCCTCTCCGCTTGCGCCAGGGCACGG
 ACCGGCCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCAG
 GACTTCAAGGCCCTCCACCAAGTCCCTGGGGGTGTCCAGGCTGCAAGTCTGTGACCCGT
 GTGCAAGCAGCGCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAC
 CATGGACCCGCTCTGCGACCAAGGAGCCCGGACCCTGCCTCGGCCACAGATGCCAC
 CATGGAATAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGGAGG
 GGACTTGTGTGACAACAAGAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC
 GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCATCATGGAATGTGCTGGGGGCT
 GTGGGCCCCAGTGCTGCCAGCCACCCGCAGCAAGCGGCGGAATACGTCTTCCAGTGCACG
 GACGGCTCCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGCGCTGCCTCGCGTGTTC
CTAAGCCCCCTGCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC
 ATGTGGGACCCCCCTGGTGATTGAGCATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAAGA
 AAGAAATATTAAGTATATTGTAATAATAACAAAAAATAGAAGTAAAAAAAAAAAAAAAAA
 AAAAAA

FIGURE 112

MAPGWAGVGAAVRARLALALASVLSGPPAVACPTKCTCSAASVDCHLGLRAVPRGIPRN
AERLDLDRNNITRITKMDFAGLKNLRVLHLEDNQSVSIERGAFQDLKQLERLRNKNKLQVL
PELLFQSTPKLTRDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCIEDGAFRALRDLLEIL
TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLQRRTVGQFTLCMAPVHL
RGFNADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
EIRLEQNSIKAIPAGAFQYKYLKRIDISKNQISDIAPDAFQGLKSLTSLVLYGNKITIAK
GLFDGLVSLQLLLLANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL
AQNPFVCDCHLKWLDYLDQNPITSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
SECFMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRNDNEVSVLEATGIFKKLPN
LRKINLSNNKIKEVREGAFDGAASVQELMTGNQLETVHGRVFRGLSGLKTLMLRSNLISCV
SNDTFAGLSSVRLSLYDNRIITITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRRR
IVSGNPRCQKPFLLKEIPIQDVAIQDFTCDGNEESSQLSPRCPEQCTCMETVVRCSNKGRL
ALPRGMPKDVTELYLEGNHLTAVPRELSALRHLLTIDLSNNSISMLTNYTFSNMSHLSTLIL
SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCSLRWL
SEWVKAGYKEPGIARCSSPEPMADRLLLTTPHFRQCKGPVDINIVAKNACLSSPCKNNGT
CTQDPVELYRCACPYSYGKDCTVPINTCIQNPCQHGCTHLSDSHKDGFSCSCLPGFEGQR
CEINPDDCEDNDCENNATCVDGINNYVICPPNYTGELCDEVIDHCVPELNLCQHEAKCIPL
DKGFSCCECVPGYSGLKETDNDDCVAHKCRHGAQCVDTINGYTCTCPQGFSGPFCEHPPPMV
LLQTSPCDQYECQNGAQCIVVQQEPTCRCPGFGAGPRCEKLITVNFVGKDSYVELASAKVRP
QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSSPPTTVYSVETVNDGQFHS
VELVTLNQTNLNVVDKGTPKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF
HGCIEHVRINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCERPGWTGFLC
DQEARDPCLGHRCHHGKCVATGTSYMCCKAEGYGGDLCDKNKDSANACSAFKCHHGQCHISD
QGEPYCLCPGFSGEHCQENPCLGQVVREVIRRRQKGYASCATASKVPIMECRGGCGPQCCQ
PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT
 CCGGCAGGCTTTGAGG**ATGA**AAGGCTGCGGGCATTCCTGACCCTCATTGGCTGCCTGGTCACAG
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAACCTGGCAAAAATATTCTCGAGGGCTGGCCTG
 GACAATTACTGGGGCTTCAGCCTTGGAACCTGGATCTGCATGGCATATTATGAGAGCGGCTA
 CAACACCACAGCCCCGACGGTCTTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA
 ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTGCGCTGC
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
 GACACAAGGAATGAACTATTGGCAAGGCTGGAAGAAACATTGTGAGGGCAGAGACCTGTCCG
 AGTGAAAAAAGGCTGTGAGGTTTCCT**TAA**ACTGGAACCTGGACCCAGGATGCTTTGCAGCAAC
 GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCTATCTTGTCGCCGTTTCCTCCAATA
 TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACCTTTTAAGAAAATAAATATTTCCAT
 TTAAATGTC

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FIGURE 114

MKAAGILTTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKCLKENNHCHVACSALITDDLTDAAICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

FIGURE 115

CAGGCCATTTGCATCCCACTGTCTTGTGTTGCGAGCCAGGCCACACCGTCTCAGCAGTGT
CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAACCTTTGTACATGGCTCCC
CATTGGTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCCACTGTTT
AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTACTGTCACTTCCCAGATCTGCTTCTCAC
CAAGAGAGATTCTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
CCACAGGCATGGCAGAGCTGCATCTTAGTCAACAGCCAGTTTACAGCTGCTGTTTTTAAGGAA
ACATTCAGTCCCTGTCTCACATAGACCCTGATGTCTCTATCCATCTCTAAATGTCACCAG
CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC
TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
TTATGACGAGAGAGTCTTGGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
AGTCCGACCTTGGCCAGTATGTGACCTTCTTGAGGTCTTTCAGACAAACAGAAAAATCTCC
CTCTCCACAGCTGCACGTGTGTGCTTTACACACCAAGCAATGAGCACTTTGGCATTGTCCC
TCTGGAAGCCATGTACATGCAGTGCCCACTATTGCTGTTAATTCGGGTGGACCCCTTGGAGT
CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCACCTTCTCAGAAGCA
ATAGAAAAGTTCATCCGTGAACCTTCCTTAAAGCCACCATGGGCTGGCTGGAAGAGCCAG
AGTGAAGGAAAAATTTCCCTGAAGCATTACAGAACAGCTCTACCGATATGTTACCAAAC
TGCTGGTAT**TAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC
CAGTTTTGAAACAAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA
CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA
AACCATGCTTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG
TCATTCCATGTTTCAGCAGAGTATTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA
TAAATTTTGAATGATACATGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA
AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCCCAAGATTCAAT
CCACCGAAGTGTTCACTGTCACTGTGTAGGGAATTTTGTGTTGCTGCTTTGCTGGATC
CATAGCGAGAGTGCTCTGTATTTTTTTTAAAGATAATTTGTATTTTGCACACTGAGATATAA
TAAAGGTGTTTATCATAAAAAATAAAAAAAAAA

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FIGURE 116

MPLLKLVHGSPLVFGEKFKLFTLVSAIPVFRLLARRRKKILFYCHFPDLLLLTKRDSFLKRLY
 RAPIDWIEEYTTGMADCILVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSDSVVPEKLD
 DLVPKGKKFLLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
 HYQELKKMVQQSDLGQYVTFLLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
 IAVNSGGPLESIDHSVTGFLCEPDVPVHFSEAIEKFIREPSLKATMGLAGRARVKEKFSPEAF
 TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACCAATGTTGGACTTCGCGATCTT
CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCAGAC
AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
GTGAATAGTGGAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCTGTGGT
CTCCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGACTGAAGCAGC
ATATCAATCCCAATAAGACATCGGACCCTTTTGAACCATGCTGAAGTCATTATTAAGGTAT
CAATCTGGTGGTGGCAGTGTGAGTGAAACCACATGAGGAAAAAATTGTATGAAAATGGTGT
GACTGATTCTCTGAAGAGTAACCTTTGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA
AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTTGCT
ATGAAGTCTGTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG
CTTCCAGAAGAATCATGGCACAGTTTGGTCTGAGATTGGAAAAGGCTTCTAGATGGGTAC
TTGATAAAAAACATGACTCGGAAAAAACAAATGAAGATGCCCTCATGCAACTGGAGTCTGTT
TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTTCAGTCAACATATTTTCATTGACTC
CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTTCTCTGG
CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTTAACCACCTCTGAA
GAAGTTCAAAAAAATTTATATGAAGAGATAAACCAAGTTTTTGGAAATGGTCTGTACTCC
AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGCAACTGCCA
AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAAATTGACCGATTTATATT
CCTAGAGAGACCTCGTCCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC
ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCCCT
CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA
GTACTTCTTAGTGTATTGGTGGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA
AACAAAGTATGAACCTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT
ATTAAATTTTTATACATTTAAATCATTGTTAAATTGATTGAGGAAAAACAACCATTTAAAAA
AAATCTATGTTGAATCCTTTTATAAACAGTATCACCTTGTAAATATAAACACCTATTGTAC
TTAA

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FIGURE 119

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA
 GACCGCCGCCCTTGTCCCCGAGGGCCATGGGGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC
 CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCAGGACAGCAACAT
 ACAGGCCTGCCTGCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTAGCTGG
 TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA
 GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT
 GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTTGTCT
 TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTCGTCACCGCTTTTGGGCTGAAA
 AAGAAACCCTTCTGATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG
 CCGCTTCGTATTCTGGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC
 TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA
 GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTTAGGGGACA
 ATTAATAAAAAAAAAA

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FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

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FIGURE 121

TCCCGGACCCTGCCGCCCTGCCACT**ATGT**TCCCGCCGCTCTATGCTGCTTGCCCTGGGCTCTCC
 CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
 GTGCCCCGGAACGAGTGAAGGCCCTGGCATCAGAGTGCGCCACGACCTGAGCCTGCCCTT
 ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC
 AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCAGCTGGGCTAC
 AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC
 CCACTCAGGTCACTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG
 ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCAGGGTCTACTGGCCTGCGGTGTGGCT
 CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC
 TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCC**TGA**GGCC
 CTGCTGATCCGCACCCCATTCCTCCCTCCCATGGCCAAAAACCCCACTGTCTCCTTCTCCA
 ATAAAGATGTAGCTC

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FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:
amino acids 1-20

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAGATGCAACT
GACTCGCTGCTGCTTCGTGTTCTCGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
ATGATGGTCTCTCCCGGCTCAGAGGACCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC
CGGGTGCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCCCCCCATGGCCAATTCCACTCT
CCTAGGGCTGCTGGCCCCGCTGGGGAGGCTTGGGGCATTCTTGGGCAGCCCCCAACCGCC
CGAACCACAGCCCCCACCTCAGCCAAGGTGAAGAAAATCTTTGGCTGGGGCGACTTCTAC
TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGAAGATTGTGGACCATGGCAA
TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCGGACCTC
GCTTTGCACCCAGACCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT
GGAGCTGCTCCCAAGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCAGCGACTAT
CGGCTGGTCCAGAAGGTGTGCCAGATTACAACATACCATAGTATACCCCTACTACCCATC
TGGGTGACCCGGGGAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCATGC
AGGAGACCATCTGGACACCGGGCAGGGAAGGGTTGGGCCTCAGGCAGGGAGGGGGTGGAG
ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGTCCCAAGTG
CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGAGTGGGCT
CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
TGTGGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT
CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTTCATCAGTGTGGACAGCCTG
TCAACTTAGGATGGATGGCTGAGAGGGCTTCCTAGGAGCCAGTCAGCAGGGTGGGGTGGGGC
CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCCCTGTGCTGTGCTGAGCATG
GCATGAGGTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC
CAGCCAGGCCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCTGTACCACCCATT
GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCTCCACACTAAGGCC
ACAGCCCATCCGCGTGTGTGTGCCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
CATCCATGTCCCGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTGACAGCGGGGTCTCTC
CGGATCTGGATGGCGCGCCCTCTCAGCAGCGGGCAGGGTGGGGCGGGGCCGGCCGAGA
GCATGTGCTGGATCTGTTCTGTGTCTGTGCTGTGGGTGGGGGAGGGGAGGGAAGTCTTGT
GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTCTTGGAGCAGGAAATAAAGCTT
GCCCCGGGGCA

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FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521

><subunit 1 of 1, 252 aa, 1 stop

><MW: 28127, pI: 8.91, NX(S/T): 5

MQLTRCCFVFLVQGSLLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNPNHSPPPSAKVKKIFGWGDFYSNIKTVALNLLVTGKIVD
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPY
YPSG

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

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FIGURE 125

GTGAATGTGAGGGTTTGATGACTTTTCAGATGTCTAGGAACCAGAGTGGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGGAGACTTTGACTTCAAGCCACAGAAT
 TGGTGGAAGTGTGCGCGCCGCGCCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGACACGGGATCCCGGGGTAGGAGGCGACGCGGGCGAGCACCAGCGCCAGCC
 GGCTGCGGCTGCCACACGGCTCACCATGGGCTCCGGGCGCGGGCGCTGTCCGCGGTGCCG
 GCCGTGCTGCTGGTCTCTACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC
 CATCGTGTCTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG
 GCTCCTCTTCTCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTCGCTTCTCG
 GCGGTGCGGAGCACCAACCAGGACCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT
 CGATCAGATCCTGGTGAATGTGGGTAATTTTTCACATTGGAGTCTGTCTTTGTAGCACCA
 GAAAAGGAATTTACAGTTTCAGTTTTACGTCATTAAAGTCTACCAGAGCCAAATCTCCAG
 GTTAACTTGATGTTAAATGGAAAACAGTAATATCTGCCTTTGCGGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGTCTGCTCTACCTAGATAAAGAGGATAAGGTTTACCTAA
 AACTGGAGAAAGGTAATTTGGTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTCTGGTG
 TTCCCCCTATAGGATTCAATTTCTCCATGATGTTATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG
 TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTCTGCAAGACTTATTCTGAATTTCAATTCCTGGGATTACTGAATTAGT
 TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACCTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAATCTGATACTG
 TGTTAATATATTGATTATATTGTTTTTATTCCTTTGGAATTAGTTTGTGGTTCTTGTA
 AAAACTTGGATTTTTTTTTTTCAGTAACTGGTATTATGTTTTCTCTTAAATAAGGTAATGAA
 TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAAAA
 GAATGCTTCATAGTTGTATTTTAAATGTATATGTGAAAGAGTCATATTTTCCAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAAATCTTATACTTTATTGC
 TCAACTTTAATTAAATGATTGATAATAACCACTTTATTAAAAACCTAAGGTTTTTTTTTT
 TCCGTAGACATGACCACTTTATTAAGTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT
 TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACTCTTTAAATTGTA
 TATATTTATCTGTTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTTAGTGAATAT
 CTGTCTTTTGTATAGTGCATATGAATTCATAAAATTTATTTATGCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

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FIGURE 126

MGSGRRALSAVPAVLLVLTLPGLPVWAQNDTEPIVLEGGKCLVVCDSNPATDSKGSSSSPLGI
SVRAANSKVAFSAVRSTNHEPSEMSNKTRIYYFDQILVNVGNFFTTLESVFVAPRKGIYSFSF
HVIKQYQSQTIQVNLMLNGKPVISAFAGDKDVTREAAATNGVLLYLDKEDKVYLKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:
amino acids 1-27

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FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCCTCATCGCCGGAGC
TTTCTTCTGGTTGGTGTCTCTACTGATTTCTGCCCTTGTTTGGTTCATGGCAAGAGTCATTA
TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT
GAAGAGTATAAACCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCTATCTGACTCCTTGGGG
CCAGGCACAGTGGGCATTCATGGAGATTCTCCTCAATTCTTCCTTTATTACGCTTTCATGAC
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGTATGGCTGTGAGAAGA
AAAAGTGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTTATAATCCTGGTGCTCATGGGCAC
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG
ACAAGAACTTTCTTTTACAACCAGCGCTCCAGAT**TAA**ACCTCAGGGAACCAGCACTTCCCAA
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTTCTGAAAAATCCCTTTTCTG
GTGGAATTGAGAAAGAAATAAACTATGCAGATA

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FIGURE 128

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGFPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLAYVSGLGF
GIMSGVFSFVNTLSDSLGPGTVGIHGDSPOFFLYSAFMTLVIIILHVFVGIVFFDGCCKKKW
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACAGCGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTTCGCTCTGGGCTTGCCCTTCT
 TGGTGCTCTTGGTGGCCTCGGTGGAGAGCCATCTGGGGGTTCTGGGGCCCAAGAACGCTCTCGCAGAAAGACGCCG
 AGTTTGGGCGCACCTACGTGGACAGGTCACACGCAGCTGGTCAACATCTACACCTTCAACCATACCTGTGACCC
 GCAACAGGCACAGGGGCTGCGTGTGCTGTGAACGCTCTGAACAGCAGAAAGGGGGCGCGCTGTGCTTTGTGG
 TCCGCGAAGAGGAGCTGTGGTGTCTTCCAGGTGCCCTAATCCTGCGAGGGATGTTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGAACGAACCTCTGTGACGCCCCCACAAGAAATGAGTCGGAGATTCAAGTTCTTACGTGGGATG
 TGTCCACCTGTCAACGATCAACACCATACACAGCTCCGGGTGAGCGCATGGACAGATTGTTGCTCAGGAGTGT
 GGGAGCAGTTTCAAGTCAATACCACAGCAGCAGCCCCAGTACTTCAAGTATGAGTCCCTGAAAGCGTGGAGT
 CGGTAAATTTGTCAGGTGACCTCCAACAAGGCCTTCCCTGCTCAGTCATCTCCATTCAAGGATGTGCTGTCTCTG
 TCTATGACCTGGACAAACAGTAGCCTTCATCGGCATGTACCAGACGATGACCAAGAAGCGCGCCATCACCGTAC
 AGCGCAAAGACTTCCCGACAACAGCTTTTATGTGGTGGTGGTGAAGAGACCAAGCTCAGCGGGGCT
 CCTGCTCTTTTACCCCTTCGCAAGAAGTGAACCGGTGATCAAGGGGACCGCCAGAAAAACCTGTCAAGTGTGG
 TGTCTCAAGCAGTCACGTCTGAGGCATACGTCACTGAGGGATGCTCTTTTGGCTGGGTATATTTCTCTCCTTTTACC
 TGCTGACCGTCTCTGCTGCTGCTGGGAGAACTGGAGGCAAGAAAGAACCTGCTGGTGGCCATTGACCGAG
 CTTGCCCAAGAGCGGTCAACCCTCGAGTCTTGCTGCTGATTCTTTCTCGGCAGTTCCCTTATGAGGGTTACAAC
 ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGGTTGACAGCGCTGGCACTGGGGACCTCTCTTACG
 GTTACCAGGGGCGCTCCTTTGAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGGATG
 ACTACGACACATGACCGCATCGATTCCGACAAGAATGTATTTCGCAACCAAGCAATACCTCTATGTGGCTGACC
 TGGCACCAGAGGACAAGCGTGTCTCGGGAAGTACCAGATCTACTTGTGAACATTTGCCAACTGTGCTGTCT
 TCTATGCCCTTCTGTGGTGCGAGCTGGTGATCACTACAGACGGTGGTGAATGTACAGGAAATCAGGACATCTG
 GCTACTACAACCTTCTCTGCGCCACCCACTGGCAATCTCAGCGCTTCAACAACATCTCAGCAACCTGTGGGT
 ACATCTCTCTGGGGCTGCTTTTCTGTCTCATCTCTGCAACGGGAGATCAACCAACGGGGCCCTGCTGCGCA
 ATGACCTCTGTGGCTGGAATGTGGGATCCCCAAACACTTTGGGCTTTTCTACGCCATGGGCAACGCCCTGATGA
 TGGAGGGGCTGCTCAGTGCTTGTCTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACACATCGTTTCATGT
 ACATGATCGCGGCCGCTGCAATGCTGAAGCTCTACCCAGAAGCGGCAACCGGACATCAACCGCAGCGCTACAGTG
 CCTACGCGTGGCTGGCCATTGTCTCTCTCTGCTGGGCGTGGTCTTTGGCAAAGGGAACACGGGCTGTCT
 GGATCGTCTTCTCATCAATCACATCACTCGCCACCCCTGCTCCTCAGCAGCGAGCTATTGACGTTGGGCGGTGGA
 AACTGGACTCGGGGATCTTCCGCGCATCTCCACGTGCTTACACAGACTGATCCGGCAGTGACGCGGCGCGC
 TCTACTGTGGACGCATGGTGTGCTGGTGTGATGGCAACGTCACTGAGTGGTGGCTGCTGCTTATGGCTTATCA
 TCGCCCCCAATGATTTCGCTTCTACTTGTGGCCATTGGCATCTGCAACCTGCTCCTTTACTTCCGCTTCTACA
 TCTATGAAAGTCCGGAGTGGGGAGAGGATCAAGCTCATCCCGCTGCTCTGATCGTTTGCACCTCCGTGGTCT
 GGGGCTTCGGGCTCTTCTTCTTCTTCCAGGACTCAGCACCTGGCAGAAAAACCCCTGACAGATCGAGGGAGACA
 ACCGGGACTGCATCCTCTCGACTCTTTGACGACCAAGCATCTGGCACTTCTCTCTCCTCATCGCATGTGTTG
 GGTCTTCTGGTGTGCTGACACTGGAAGACGACCTGGATAGTGTGACGCGGGAAGATGATGCTTCTTAGC
 AGGAGCTCCGCTTGGCTTCACTCAAGGGGCGCTGAGCTCCTTTGTGTATACACCGGTGCTATCTGTGCTGT
 GTGGGATGAGTCCAGCAGCCGCTGCCAGCAGTGGATGGCAGCAGGACAGCGGTGCTAGCTTAGGCTTGGCT
 GGGACAGCATGGGGTGGCATGCTGAGCTTGCAGTGGCTTGGCGAGCGAGCGCTGCTCCCTGGAAACCC
 AGATGTTGGCCAAATGCTGCTTTTCTCAGTGTGGGGCTTCCATGGGCGCCTGCTCCTTTGGCTCTCCATTT
 TGCTTTTGAAGAGGAAGGATGGAAGGACACCCATCCCCATTTCATGCTTGCATTTTGGCGTCTCCTCCCC
 ACAATGGCCCCAGCTGGGACCTAAGGCTCTTTTCTCCCATCACTCCCCTCAGGGGCTAGTCTGGGGCTGTA
 ATCTCTGTCGTATCAGGGCCCCAGTCTCTTTGGGCTGCTGCTGCTGCTCATCTGCCATTCAAGTACGCTGAGC
 AGGATGGATGGGGGTATGAGATTTTGGGGGTGGGCGAGCTGGTGCCAGACTTTTGGTGTGAAGGCTGCAAGGGG
 CTTGGGGCAGTGGGATTTCTTCTCCTCTGACCTGTGCTCAGGGCTGGCTTTTGGCAATGCTGCAAGCCCAAT
 TGAAGACCGCTCTGATTCAAGAGGCTGAATCAGAGGTCACCTCTTATCCCATCAGCTCCGAGCTGATGCC
 AGCACCAGGATGAGAGGGAAGCGGCTCACCCCTTCCCTTCTTCCAGGGCTTACGCTTGTGCCAAACCC
 AGCTGTTGGGCTTTCAAGTGCCATTGACACTGCCCAAGATGTCCAGGGGCAAGAGGGGATGATACAGAGCTCAG
 CCCTGTTGCTCCACAGCTGTGGGCAACCCAGTGCTTACCTTGAAGAAGGGCTCAGGAAGGATGTGCTGTT
 CCCTCTAGCTGGCGAGTCTAGCTCGCTCTAGGACCCAGGGCTGGCTCTAAGTTTCCGTCCAGTCTTCCGCA
 AGTTTGTGTTAGTCATCAACACATACCTATGAACCTTGAAGTTTACAAGAAATGCCCAAGCTCTGGCAG
 CTTGGCCACCTTGCTCTTGGATCCCTTCTGTCACCACTGGTCCACCCAGATGTGAGGATGGGGGCTCAGG
 CGGGGCTCTCCTTCTGGGATGGAAATGTTTTTCTCCAACTGTTTTTATAGCTTCTGCTTGAAGGCTGGG
 AGATGAGTGGGTCTGGATCTTTTCTCAGAGCTCTCCATGCTATGTTGCTATTCCGTTTTCTATGTAAT
 TGCATTCAATAAACACCGACTCAAAAAAAAAAAAAA

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FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1' of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
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EGVRVSVNVNLNKQKAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYDLNNAVAFIGMYQTMTKKAAITVQRKDFPNSFYV VVV
VKTEDQACGGSLPFYPPFAEDEPVDQGHRQKTL SVLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDL SYGYQGRSFEFVGTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTKQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVNVVTGNQDICYNFLCAHPLGN
LSAFNNILSNLGYILLGLFLLLIILQREINHNRALLRNDLCALECGIPKHFGLFYAMGTALM
MEGLLSACYHVCPTYNTNFQFDTSEFMYIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLSTQLYYMGRWKLD SGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGFALFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTDDDLDTVQRDKIYVF
```

Important features of the protein:

Signal peptide:

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTGCCTTGCCCCACCCAGCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGTCTTGGCAGCTGGACCAAGGGAGGCCAGTCTTTGGGCGCTGGAGGGCCGTGCTCTG
 ACCATGGTTCCTGCTGCTGGCTGTGGCTGCTTTGTCTCCCGTCCCCAGGCTCTCCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCCAGAAAATATGGTGGAAATTTCCCTTTATACC
 TGACCAAGTTGGCCGCTGCCCGGTGAGGGGGCTGAAGGCCAGATCGTGCTGCAGGGGACTCA
 GGCAAGGCAACTGAGGGCCATTGTCTATGGATCCAGATTCTGGCTTCCTGCTGGTGACCAG
 GGCCCTGGACCCGAGAGGAGCAGGCAGAGTACAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGCTTGTGGGTCCACAGCCTGTGCTGTGCACGTGAAGGATGAGAATGACCAAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTCGGCTGAGCCGGGGTACCAGGCCCTGGCATCCC
 CTTCTCTTCTCTTGAAGGCTTACAGACCGGGATGAGCCAGGCACAGCCAACTCGGATCTTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCAGCCTTCCCCAGACATGTTCAGCTGGAGCCTCGG
 CTGGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACCAGCCTTGACCACGCCCTGGAGAGGAC
 CTACCAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCCTCAGGCCACCAGGCCACTG
 CCACCGTGGAACTCTCCATCATAGAGAGCACCTGGGTGTCCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCCCTATACCCGCAACACATGGCCCCAGGTACACTGGAGTGGGGTGATGTG
 GCATCTACCTGGAGGCCATCCCCCGGGACCCCTTTGAAGTGAATGCAGAGGGGAACTCT
 ACGTGACCAGAGAGCTGGACAGAGAAGCCCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCTTGGCGAGGACTATGCGGCCCTCTGGAGCTGCACGTGCTGGTGATGGATGAGAA
 TGACAACGTGCCATATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGCAGTACTGTACAGCAGAGGATGCAGATGCCCCGGGCTCCCCAATTCC
 CACGTTGTGTATCAGTCTCTGAGCCCTGAGCCTGAGGATGGGGTGGAGGGAGAGCTTCCA
 GGTGGACCCCACTTCAGGCAGTGTGACGCTGGGGTGCTCCCACTCCGAGCAGGCCAGAACA
 TCCTGCTTCTGGTGCTGGCCATGGACCTGGCAGGCGCAGAGGGTGGCTTCAGCAGCAGCTGTG
 GAAGTCGAAGTCGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACTTCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCCCGGGACTCTGGTGGCCATGTAAACGCCA
 TTGATGCTGACCTCGAGCCCCGCTTCCGCTCATGGATTTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTTGGCCTGGATTGGGAGCCAGACTCTGGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGGTGCAGAGTGTGGCGA
 AGCTGGTGGGGCCAGGCCAGGCCCTGGAGCCACCGCCACGGCTGACTGTGCTAGTGGAGAGA
 GTGATGCCACCCCCAAGTTGGACCAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGGCCCC
 AGCCGGCTCTTTCTGTGCTGACCATCCAGCCTCCGACCCCATGACCGCAACCTCAGGTTCT
 CCCTAGTCAATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTTCCGGGGAGGTGCACACC
 GCCCAGTCCCTGCGAGGGGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCAGGA
 TACAGGGGCGAGTGCATTCGCTTGTGCCCTTCCCAATACCTCTGCACACCCCGCAAGACCATG
 GCTTGATCGTGAGTGGACCCAGCAAGGACCCCGATCTGGCCAGTGGGCGACGGTCCCTACAGC
 TTCACCCTTGGTCCCAAGCCACGGTGCAACGGGATTGGCCCTCTCAGACTCTCAATGGTTT
 CCATGCCTACCTCACCTTGGCCCTGCATTGGGTGGAGCCACGTGAACACATAATCCCGGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCCTGGTTCGAGTGATCGTGTGTGCTGCAAC
 GTGAGGGGCGAGTGCATGCGCAAGGTGGGCCGATGAAGGGCATGCCACCGCAAGCTGTCCGC
 AGTGGGCATCTTTGATGCCACCTGGTAGCAATAGGAATCTTCTCATCCTCATTTTCACCC
 ACTGGACCATGTCAAGGAAGAGGACCCGGATCAACAGCAGACAGCGTGGCCCTGAAGGCG
 ACTGTCTGAATGGCCAGGCAGCTCTAGCTGGGAGCTTGGCCCTTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGCCCAAGTCCAGCAGGGGACAGGACAGAGTGAAGGCCCTCCAT
 CTGCCCTGGGGTGGAGGCACCATCACCATCACAGGCATGCTCAGAGCGCTGGACACCAAC
 TTTATGGACTGCCCATGGGAGTGCTCCAATGTGAGGTGTTTGCCCAATAATAAAGCCCCA
 GAGAAGTGGGCTGGGCCCTATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAG

FIGURE 132

MVPAWLWLLCVSPQALPKAQPaelSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAEYQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQFSPDMFQLEPRL
 GALALSPKGSTSLDHALERTYQLLVQVKMDGDAQSGHQATATVEVSI IESTWVSLEPIHLAE
 NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLAEDADAPGSPNSH
 VVYQLLSPEPEDGVEGRAQVDPTSGSVTLGVPLRAGQNI LLVLAMDLAGAEGGFSSTCE
 VEAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTADADLEPAFRLMDFAIERGDTE
 GTFGLDWEPDSGHVRLRLCKNLSYEAAPSHEVVVVQSVAKLVGPGPGPGATATVTVLVERV
 MPPPKLDQESYEASVPISAPAGSFLLLTIQPSDFISRTLRFSLVNDSEGWLCIEKFSGEVHTA
 QSLGQAQPGDITYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRQLQTLNGSHAYLT LALHWVEPREHIIPVVVSHNAQMWQLLVIVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGT LVAIGIFLILIFTHWTMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTGAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT
 TCAATCGGCCCTGTGGATGTCTGGTCCCATCTGTCAAGTCTGCAGGCATTTAAATCCTTCTGT
 AGATCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTTTAGACAATGA
 AGATGATGAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAAATCAACTCAACTACGGGG
 CTTACCATTCCCTGGAAGCTATTTACCACGAGATGGACAACATTGCCGAGACTTTCTGTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTCGTTGAAAAACCGGCCGATGTATGTACTGAAAGTT
 CAGCACTGGGAAAGGCTGAGGCGGCCGCCGTTTGGCTGAATGGAGGCATCCATTCCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAAGAG
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGCGCTGTGGCCAAATCC
 TGTATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGGGTCCCGAAATC
 CTGGAAGCTCCTGCATTGGTGCTGACCCAAATAGAAAATGGAACGCTAGTTTTGCGAGGAAAG
 GGAGCGAGCGACAACCCCTTGCTCCGAAGTGATCCATGGACCCACGCCAATTCGGAAGTGGA
 GGTGAAATCAGTGGTAGATTTTCATCAAAAAATCGGGAATTTCAAGGGCTTCATCGACCTGC
 ACAGTACTCGCAGCTGCTGATGTATCCATATGGTACTCAGTCAAAAAGGCCCCAGATGCC
 GAGGAACTCGACAAGGTGGCGAGGCTTGGCGCCAAAGCTCTGGCTTCTGTGTGCGGCACTGA
 GTACCAAGTGGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG
 CGTATGACAACGGCATCAAAATTTGCTATTGAGTTGAGTGTGAGAGATACCGGGACCTATGGC
 TTCCCTCTGCCAGCTAACCAGATCATCCCCACTGCAGGAGGACGTGGCTGGGGCTGAAGAC
 CATCATGGAGCATGTGCGGACAAACCTCTACTAGGCGATGGCTCTGCTCTGTCTACATTTAT
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTCTCTACCTGTGTGAG
 TCAGAGCCCTCTGGGTTTTGTTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT
 CGTGTGTCTTGGCGGTGTCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTTTGGTCCCTG
 CTGTTTTTGTATGAGCCTTTTGTCTGTTTCTCCTTCCACCCCTGCTGGCTGGCGGCTGCACCT
 AGCATCACCCCTTCTCGGTGGCATGTCTCTCTACCTATTTTAGAACCAAGAACATC
 TGAGATGATTCTCTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCCTGTTGGTGCAC
 GTGGGAGACCACTTGTCTTTAGGTGGGTCTCAAGATGATGTAGAATTTCTCTTAATTTCT
 TCGCAGTCTCTTGGAAAAATATTTTCCCTTTGAGCAGCAAACTCTGTAGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTCTCTGTTTTTTTTTTTTTTTGGAGACAGATTTTGTCTTGTGTGCC
 CAGGCTGGAGTGTGATGCTGATCTTGGCTCACCACAACCTCTGCCTCTGGGTTCAAGCA
 ATTCTCTGCTCCTCAGCCTCTTGAGTAGCTTGTTTTATAGGCGCATGCCACCATGGCTGGGCTA
 ATTTTGTGTTTTTAGTAGAGACAGGGTTTCTCCATGTTGGTCAAGCTGGTCTCAAATCTCCCA
 ACCTCAGGTGATCTGCCCTCTTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCGGGGCCGTCCTCTCTTTTATTTAGGCTGAATACAAAGTAGAAGATCACTTCTCTTCC
 TGTCTGAGAATTTCTGATTTACTACAGTTCTTACTCCTCTCTTCCCTTTGTTATTACGTGTG
 ACCAGGATGGCGGGAGGGGATCTGTGCACGTGAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTGCAAGTGGTGAAATTTATCCCCATCTGTCTTAATGGGCTTACCTCCT
 CTTTGCTTTTGAACCTCACTTCAAGATCTAGGCCTCATCTTACAGGCTCTTAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCCATTTGTGCTGTGGTGTATCCTGTGTT
 TCTTGTCTCTGGTTTGT
 TCTGTCTATTTTGTATCCTGGACCACAAGTTCTTAAGTAGAGCAAGAAATTCATCAACCAGCT
 GCCTCTTGTGTTTCATTTACCACTCAGCAGCTACCATCTGTCTTTTGTGTTGTGTTGTTGTT
 TTGTTTTTTTGTCTTTTACCAACATGTCTGTAAATCTTAACCTCTGCTAGGATTTGTACA
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

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FIGURE 134

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEAYVTIEDLQALLDNEDDEMQHNEGQERSNNFNFGAYH
SLEAIYHEMDNIAADFPLARRVKIGHSFENRPMYVLKFSTGKGVRPPAVWLNAGIHSREWI
SQATAIWTARKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPTAEETWLGLKTIMEHVRDNLV

Signal peptide:

amino acids 1-16

[illegible]

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FIGURE 136

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP
SKDLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQCK
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMHQKEQFAF
GVDTELNCFVLQMDYKGDVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

[illegible]

FIGURE 138

MKMQKGNVLLMFGLLLHLEAATNSNETSTSANTGSSVISSGASTATNSGSSVTSSGVSTATI
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTTSSGASTATNSE
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS
TTSSGASTATNSESSTTSSGASTATNSESSTVSSRASTATNSESSTTSSGASTATNSESRTT
SNGAGTATNSESSTTSSGASTATNSDSSVTSSGASTATNSESSTTSSGASTATNSESSTSS
GASTATNSDSSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTTSSGA
NTATNSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTATNSDSSSTSSEAST
ATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTSSAGSGTAALTGMHTTSHSASTAV
SEAKPGGSLVPWEIFLITLVSVVAAVGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP
GPGGNHGAHRPRWSPNWFWRRPVSSIAMEMSGRNSSGP

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC
CCAGCAAT**ATGC**ATCTTGCACGCTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC
CTGTCTGGATGGGCGGCCAGCGATGACCCCATGAGAAGGTCATTGAAGGGATCAACCGAGG
GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAAATCACGC
ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGC
AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT
CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG
CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCAC
CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGTCAACCATGCTGCTGACCAGGCTGG
AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC
AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG
GGCCTCAGTCAACACGCCTTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCA
TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC
ATGACCTGGAGGGGTGGGGGTGGGGACAGGTTTCTGAAATCCCTGAAGGGGTTGTACTG
GGATTTGTGAATAAACTTGATACACCA

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FIGURE 140

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><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGLSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHGTGKELDKGVQGLNHGMDKVAHEINHIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTFFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

CTCCGGGCTCCACGGGGCTCCGGCCGGGGCCGCTGGCCGGGGGACGAGTCACTGGACACTCAGAGAGCGGCC
CCGGGGGGGGCGATGACCTGCCTGACCTCACTCACTCACTCCGAGCGGGGGGGCCCGGGGGCGCATCTG
GGGGCGGACCTCCGGGGCGAGCTGCCCGCTGAGTCCGGCGAGGACCTCACTGACCGCGAGCCCGGGGACACCTGC
GCTCTCTGTTCTCCGACAGTCTGCCACCGCATGGGCTGAGGAGTGGTCTGCCCGCCCTGGGGCGCTGCGC
CTCTCGGCACCCCTGCTGCTGCTCTCTGCTGCTGCTGCTCTGCTGACGCGCGCGCTCCGACCTGGGCGCTCAGC
CCCCGATCAGCGTGTCTGGGCTGTGAGAGCGGCGCATCTCTCAGATTCAAGAGTCAACACTCTCCCAATAC
ACAGCCCTTCTGTGACGAGGATGGAGGACGACCTCTAGCTGGGTGCTCGAGAGGGCCCTTTTGCATCTCAGTAGC
AACTTCAGCTCTCTGTCAGGCGGGGATACAGGAGCTGCTTTGGGTGGAGACGAGGAAGAAGAACAGTGTG
AGCTTCAGAGGCAACAGCCACGAGCGCATGTGCAAACTACATCAAGATCTCTCTCGCGTCAAGCGAGCTCAG
CTTGTCACTCTGGGACACGAGCTCTCAGCCCGATGTGTACTACATCAACATGAGAACTTCAAGCTGGGAAG
GACGAGAAGGGGAATGTCTCTTGGAAATGGCAAGGCGGTGTCTCTTGCACCGAAITTCACCTCACTGCC
TGTGGTGTGATGGGAGAGCTCTACATGGAAAGTACGACGATCTCAAGGAAATGACCGCGGAGCTCTCGGAGGAC
CAAGCGTCTCGCCCAACAGACGAGAGTCTCTCACTGGTCAAGAGCCAGTTTGTGTGCCCTACGCTAC
ATTCTCTGAGAGCTGGGCGATGTGAAGAGGATGATACAGATCTCAATTTTCTCAGGAGACTGGCCAGGAA
TTTGTAGTTCTTGAGAACAACATTGTGTCCGATTGCCCGATTCTGAAGGGGATGAGGTGGAAGAGGGGTG
CTACACAGCGGCTGGACCTCTCTCTCAAGGCCAGCTGTGTGCTCTCAGCGCCGACAGTGGCTTCCCTTCAAC
GTGCTCAGGATTTCTTCAAGTCAAGCCACGCCAGGAGTGGGTGACACTTTTCTAGGGTCTTCACT
TCCGCTGGGACGAGGGAATACAGAGGCTTCTGCCGTCTGTGCTTCAAAATGAAGATGTGAGAGAGTCTTCA
AGCGGCTCTACAGGAGGTGAACGTGTGAGACACAGCTGATGACAGCTGACCCAGCCGGTGGCCACACCCGG
CTTGAGGCTGCATCTACCAAGATCGCCGGGAAGAAGATCAACTCTCTCTCAGCTCCGACCGAGCGGTGCTGT
AACTTCTCAAGGACACTTCTGATGGACGGGCGAGTCCGAAGCGCATGCTGCTGTGACGCCACGAGCTGCT
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GGCCGCTTCCAAAGAGTCAAGTGAAGTGGCCGCCGGGTGACATCTTAGGAGCTGCAGATCTTCTATCGGGA
CAGCCGCTGCGAATCTCTCTGGACACCCACAGGGGGTGTGTTCTAGGCGCTACACTGGGCGATGTACAG
GTGCCATCGCCAACTCAGGCTGTACCGAGTCTGGGAGTGGCTCTGCGCGGGAGCCCTACTGTGGTGTGG
AGGCGCTCCAGTGCAGAAGCACTGACCTCTACCGAGCTCAGTGGCCACAGGCGTGATCCAGGACATCTGAG
GGAGCAGCGCCAAAGACTTTGACGGCGTCTTGGTTGTGTCGGCTCTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTGTCAAGTTCAGCCCAACACAGATGAACACTTTGGCTTGGCCCTCTCTTCAACTCTGGGACCGGA
CTCTGCTTACGCAACGGGGGGCCCTGCAATGCTCGGCTCTGCAAGCTGTACCCACTGGGACGCTGTGTGCT
GTGGGCAACCCAGTCTGGGGAGTTCCAGTCTGTGTCTAGAGAGGGGCTTCCAGACGCTGTTAGGCCACTAC
TGCCAGAGGTGTGTGAGAGCGGGGTGCGAGACAAACAGATGAGGTTGGAGTGTACCGCTATTATTACGACA
TCCGCTGTGAGTGCACCACTGGTGGCAAGCGGCACTGGGTTGCAGACAGCTCTAGGAAGAGTTCCTGTGCT
ATGTACAGCTCTTTGTGTGCCGCTGTGCTGCTCAAGTTTATTCTTGTCTACCGGACCGGAACAGTATGAA
GTCTTCTGAAGCAGGGGAATGTGTCAGGCTGTGCCACCGAGACTGCGCTTGGTGTGCTCCCTCTGAGCCGCG
CCACTCAACCGCTAGGCGCCCTAGACACCGGCTCGATACCGAGGGTACCAGTCCCTGCAGACAGCGCCCCG
GGGGCGCGAGTCTTCACTGAGTCGAGGAGGAGGCCACTCAGATCAAGACAGCTCTGTGGAGTATACCCAGTGT
TGCCCGCGCGGGGTGCGCTTGGCTCGGAGATCGTGACTGTGTGTTGTGAGAGCTCTCCAGAGGAGCT
TGCCCTGTCCTCAGGGGCTGTGAATCTCTGGAGAGGCTCAACTGGAACCTCCCTCGCTCTCTGTGGAAAC
ACAGCCTGTGTGCGCGGCTTGGGAGCTTGGAGCGAGTGGCCTGTGCTGTCAAGTACAGTAGCGAGGACTCC
TACCCACCGACATCAACACAGCGCTGGCCCGAGAGTCTGGCCAAATATGGGGGAGCTGCTAGTTTGGTGAA
CAGTGCCTTGTGTAATCTAGGCTTTTGTTTAAAAAACATCAAAATGTGAACTAGTAATGAGGAGGAAG
ATGATCGGCATGACGACACACAGCGTGTCTCAGTTCTAGGCTCCAGGGGTGCTGGGATGAGTCCAAATGTC
TTGCTGAGACAGATTTGGAACCTTCAACACTGGCTCTTCACTTCCAACTATTCCGCTGCCACCGGCTGCG
CTGTCTCACTCAGATCAGGACAGCGTGGGCTGGGTCGGTGTGCTGCTCGGCACTCAGCGAGGATGTAGTTG
TTGCTGGCGTCTGCCCAACTCAGGACACAGGCGGCTAGTTGGCATCGGCCCTCCAGGTTCTGGGCTG
GGACCGCACTCTGGACCTTTCAGGCTGTATCAGGCTGTGGGCCACAGGAGGACAGCGGAGCTCAGGAGA
TTTGTGCAATCTAGCCTTTCTCTCAAGATCAGGGAAGACTGTGCGCTGCTTCTCTGTTTGTGCTGTA
GAACCCGTTGGCCCTTCCCACTTATCCCTCGCTCACTTTTGACATCAACACAGGAACATACTGACGC
CTGGTCTCTCCCGAGTCCCACTTCACTCTCCTCTCACTTCTCCACTCAAGGATATCAACAGCTGCC
AGCACAGGGCCCTGAATTTATGTGTTTTTATACATTTTAAATAGATGCATTTATGCTATTTTAAATAAA
GCTCGAAGAACTACTGTTTAAAAAAAATAAA

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FIGURE 142

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLEDDGKGRCP
FDPNFKSTALVVDGELYTGTVSSFQGNDDPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFPFNVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTGSAVCVFTMKDVQRVFSG
LYKEVNRETOQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLLQPQARYQRVAVHRVPLGHHTYDVLFLGTGDGRLHKAVSVGPRVHIIIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSPLYQP
QLATRPWIQDIEGASAKDLCSASSVVSFSFVPTGEKPCEQVQFQPNVTNTLACPLLSNLATR
LWLRNGAPVNASASCHVLPTGDLLLVTGQQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECASVHPKTCPVVLPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSEKR
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSV
```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCGGAGGATGTGCAGCTGCGCGCGCGCGCGGTACGAAGAGGACGGGGACAGGCGCGGTGCGAACCGA
 GCCCAGCCAGCCGAGGAGACGCGGCGAGGGCGGGACGGGAGCCGGACTCGTCTGCGCGCGCGGTGTCGCGCGTCTG
 TGGCGCCCGCGCTCCCCGCGCGAGCGGGAGGAGCGCGCGCCACCTCGCGCGCGAGCGCGCGCTAGCGCGCGC
 CGGGCATGTGTCCTCTTAAAGGCGCAGCGCGCGCGCGGGCGGGGTGTGCGGAACAAAGCGCGCGCGCGGG
 CTTGCGGGCGGTCTGGGGGCGCGCATGGCGCGCGGGGCCCGCGCGCGCGCGCGCTGCCGGCGGGGCTCTCG
 CGCGCTTAGGGCGGGCTGCGCTCCTGTGGCGGGGGCAGCGGGCTGAGGGCGCGCGGAGCTCGCGCGCGCGGGC
 GGGCGCGCGCGCGCGCGCGGGCGAGCGCGCGCGGGC**CTGGC**CGCGCGCGCGCGCGCTGGCTCAGCGTGTG
 TGCTCGGGCTCGTCTGGGCTCTGTGCTGGGCTCGCGGCTCGTCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
 GCCCAGCGCGCGCGCGCAGCCCGAGGGCTGCCGCTCCGGGACGGCGCGGCTTCCGAGCGCGCGCGGGCGCGG
 CGCATGCGCGCGGGGCGCAGCTCTGGCGCGCGGGCTCGGACCCAGATGGCGCGCGCGCGAGCGAACTTCTCT
 TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCGTGGCGCTACAGAACATGGTCCAAGACAA
 TTCTGGGAAAGTTCACTTCTTCAAGTGAGGGTCTGACACATCTGTACCAATTCAGTAGTGCACTACGGG
 GTGTGGACGACTCTACCGCGCCCGAGAAGAAGTCTTATGATGCTCAAGTACATGCACGCCACTACTGGACA
 AGTATGAATGGTTTATGAGAGCAGATGATGACGTGTACATCAAGAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
 TGAACAGCAGCGAGGCCCTCTTTCTGGGCAGACAGGCTGGGCACACGGAAGAAATGGGAAACTGGCCCTGG
 AGCCTGGTGAGAACTTCTGATGGGGGGGCTGGCGTGATCATGAGCGGGAGGTGCTTCGGAGAAATGGTGCGCG
 CAGGGGTGCAGTGTGTCTGGTCTTATGAGATGCGGCAGCTTTTTTATGAGAATTACGAGACCAACAAAGGGGT
 ACATTAGAGATCTCCATAACAGTAAATTCACCAAGCTATCACATTACGCCCAACGAGGACCAACCTTACGACT
 ACAGGCTCCACAGCTACATGCTGAGCGCAAGATATCCGAGCTCGGCATCGCACAAATACAGCTGACCGCGGAA
 TTGTCCTGATGAGCAAAATACGACACAGAAATTCATAAGAGGACCTCCAGCTGGGAATCCCTCCCTCTCTA
 TTGAGTTTCAGCCCCCGCAGGAGAGGAGATTCGGAATGGGAGTTTCTGACTGGAAATGTTGATTGCGGAG
 TCGAGCGCCAGCCCCCTCAGGAGGAATGGACTCGCGCAACAGGGAAGCTTGAGCAGACATTTGATCAGGCTCA
 TGGAGATGATCAATGCCACGCCAAGACAGAGGGCGCATCATTGACTTCAAAGAGATCCAGTACGGCTACCGCG
 GGGTGAAACCCATGTTGGGCTGTAGTACATCTTGACCTGCTCTTCTACAAAGAGCAAGAGGAAAGAAA
 TGACGCTCCCTGTGAGGAGCGACCGGTATTTCAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAG
 TGGATGCACAAGAGTTGGCCAAAGAAATCAATCAGGAATCTGGATCTTGCTCTTCTCTCAAACTCCCTGAAGA
 AGCTCGTCCCCTTTCAGCTCCCTGGGTGGAAGAGTGAGCACAAGAACCCAAAGATAAAGAACTAAACATCTA
 TTCTTTGTCTGGGCGTTTGACATGTTTGTGAGATTTATGGGAACTTTGAGAAGCGTCTTATCCCAACT
 AGAACGTCAAGCTCGTGGTCTGCTTTTCAATCTGACTCCAACCTTGACAACCGCAAGTTGAAGTATGATGA
 GAGATTACCGCATTAAGTACCTTAAAGCCGACATGAGACTTTTGCTGTGTCTGGAGAGTTTCAAGAGCCCTGG
 CCGTGAAGTAGGATCTCCAGTTTAAACATGAATCTTTGCTCTTCTCTGCGAGCTGACCTCGTGTTACTA
 CAGAATTCCTTCAGCGATGTGAGCAAAATACAGTTCTGGGCCAACAAATATTTTCCAATCATCTTCAGCCAGT
 ATGACCCAAAGATTGTTTATAGTGGGAAGTTCACAGTGACAACCAATTTTGCTTCTGACAAAGACTGGCTTCT
 GGAAGAACTATGGGTTTGGCATGCTGTATTATTAAGGGAGATCTTGTCGAGTTGGTGCGCTTGTATGTTTCCA
 TCCAAGGCTGGGGGCTGGAGATGTGGACCTTTTCAACAAAGTTGTCCAGGACGTTTGAAGAGCTTTAGGAGCG
 AGGAAGTAGGAGTAGTCCAGCTCCACCATCTGTCTTTTGTGATCCCAATCTTGACAGAACTGACAAAAATGT
 GCTTGGGTCCTCAAGCATCGACCTATGGGTCCACCCGAGCAGCTGGCTGAGATGTGGCTGGAAAAATGATCAAA
 GTTACAGTAAAGCAGCAATAATATGGCTCAGTGAGGACAGCG**CTAAT**GTCCAGTGTGCTGGTGGAAAGAGCTTTT
 TAATTAATCTAATTTATTTTTCAAAAATTTTGTATGATCAGTTTGAAGTCGGTATACAAAGATATATTTTAC
 AAGTGTGTTTCTTACATAGGACTCCTTTAAGATTGAGCTTCTGAACAAGAGGATGATCAGTGTTCCTTTGAC
 CACATCTCTTGTGTAACATTTATGACAGACCTGCTTAACTTTGACCTGAAATGTACCTGATGAACAAACTTT
 TTTAAAAAATGTTTCTTTTGGAGACCTTGTCTGACGATCTCTATGGCAGAAACGTGAAACCTTCTGCAAGCAT
 TATTTGACAAACACTGTAACCTGTGTAATGTCTGTGTGATTTTAACTTCCACAGATTCTACCTTTTGT
 GTTTTGTATTTTCTTTTAAACATTTGTTTAAAGCCATTTTCAATGCTTCCAGTTGAAGATAGGAAATGTATATA
 CGCTGTTTCATCATTTGCTCAGGAGAGCTTCCAGAGTTGATCTTCTCTCATGGTACTCTGCTCAGCATGGC
 GAGCTAGGTTTGTGTTGTTTGTGTTTGTGTTTCTTTTGGACGGAGCTCACTCTTACCCAGCGCTGGAAAT
 CAGTGGCGCAATCTTGGCTCACTTTAACTCCACTTCCCTGGTTCAAGAACTCCCTCGCTTGGCTCCCGAGT
 AGCTGGGATACAGGCACACACACCCAGCCAGNTAGTTTGTATTTTATGAGAGAGGATGATCAGTGTTCCTGAT
 GCAAGCTCAGCTGGCCACGATGGTTTAAAGCAAGGGCGTGAAGAGGCACGTGAGGATGTGGGCTCTCTCG
 TGGTAGTTTCTCGGCTAAATAGACTGGCATTTAAATTTCAAGAGGATTTGGCATTTCTCTCTGACGCTTT
 CTCTTTAAAGGCTAAAAATTAATGTTTGAATGACAAAGATGAATTTTACAATTAATCTGATGTACACAGACT
 GAAACATACACACATACCCCTAATCAAAACGTGGGGAATAATTTGTTGTTTGTCTTTCATCTGCTGTG
 TGTATTTGGGTGGAGATGGTTTCATTCTTTCATTACTGTTTGTGTTTATCTGTTGATCTGTAATCTTTAA
 TTTATTTAATATCTGTTGTTGAGCTCTGCCATTTCTGATACCTGTATGATGATTTATTTGTTGATACCG
 GAGTGTGTTTGTGTTTATTTGTCAGTAAACCGATCTCAAGAAATTTCTTTTGGAAACGCTTTTCCCTCTCG

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FIGURE 143B

TTAATTTTATATTCTTACTGTTTTACTAAATATTAAGTGTTCTTTGACAATTTTGGTGCTCATGTGTTTGGG
GACAAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATCTCAGATCAAATGTGCCTTAATAAATTTGTT
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAAACACGTCATTGGAGGGCTGCGTATTTGTAAATAG
CCTGATGCTCATTGGAAAAATAAACCACTGAACAATATTTTCTATTGTACTTTTCGAACCATTTTGTCTCATT
ATTCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAACTTAAACACGAAAAA

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FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWLSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLVGVMTAQKYLQTRAVAAYRTWSKTIPGKVQFFSSEG
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSRVLRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCWVSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEE
ILEWEFLTGKYLYSADVGGPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPYGAEYILDLLLLYKKHKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFSLNSLKLVPFQLPGSKSEHKPEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPDNDHFAFT
QKTGFWRNYGFGITCIYKGDVLRVGGFDVSIQGWGLEDVDLFNKVVQAGLKTFRSQEVGVVH
VHPVFCDPNLDPKQYKMLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC
TTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTGCATGGCAGAGTGCT
ACGGACGACGCCT**ATGA**AAGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGTCTG
TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA
CAAGTTTTAGAGAACCTAGTACGAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC
TAACCTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAATTTAAGGAGCTAGTTA
CACATGGAGACGCTTCAACTGAGAATGATGTTTAAACCAATCCTATCAGTGAAGAACTACA
ACTTTCCCTACAGGAGGCTTACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC
ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG
AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG
TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTAC
CACTTTAGATAAAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
CAGGTGAAACTGCGATAGAAAAACCCGAAGAGTTTGGAAAGCACCCAGAGAGTTGGAATAAT
GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGA
CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC
TTGCTCTAGCAGCAGCAGCAGAACATAAATTA AAAACAATGTATAAGTCCAGTTATTGCCA
GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTAACATGCTGTGTAATTC
TAGATCTAAACTCTATGAATATTTAGATATTAAATGTGTTCACCAGAGATGAGAGAAAAAG
CTGTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA
AAAGTTTAT**TAA**ACAATAATATAAAAAATTTTAAACCTACTTGTATTCCTATAACAAAGCTGA
TTTAAGCAAACTGCATTTTTCACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT
AAAAATATTTTCTATTGTAGTTCAAATGTGCCAACATCTTTATGTGTCATGTTTATGAACA
ATTTTCATATGCACTAAAAACCTAATTTAAAAATAAAATTTTGTTTCAGGAAAAAA

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FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRVSPSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISEETTTFTTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEPEYIENEEPEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYSQLLFPVGRTSNKIDDIETVINMLCNSRSKL
YEYLDIKCVPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

FIGURE 147

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCACA
 GGAATATCC**ATG**GCCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGACA
 GTGGCAAGTCACTGGACCGGGCAAGTTTGTCCAGGCCTTGGTGGGGAGGACGCCGTGTCT
 CCTGCTCCCTCTTTCTGAGACAGTGCAGAGGCTATGGAAGTGCGGTTCTTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGAAGACTGGAACTCTAAGCAGATGCCACA
 GTATCGAGGGAGAAGTCTGAGTTTGTGAAGGACTCCATTGACAGGGGGCGTGTCTCTTAAGGC
 TAAAAACATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTTCAGTTCACGATTTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCCTCTATTTCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTGCTTCAGACTCCAGAGCAAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAAATGCTGGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTTCAGCCCTCACCTTGGCGCCTGGCTTCTATTTCCTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTCTATGGGGATGATAATTGTTTTCTTCAATCCAAAGGGAAAAATCCA
 GGCGGAAGTGGACTGGAGAAGAAAGCACGGACAGGCAGAAATTGAGAGACGCCCGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGGAC
 AAAATGTAGGGTGGTATGTGGGAGTGTGTCCGGATGACGTAGACAGGGGGAAGAACAAATGTG
 ACTTTGTCTCCCAACATTTGGGTATTTGGGTCTCAGACTGACAACAGAATTTGTATTTCAC
 ATTCAATCCCCATTTTATCAGCCTCCCCCCCAGCACCCCTCCTACACGAGTAGGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC
 CTGCTGACATGTCAAGTTGAAGGCTTGTGAGACCCATATATCCAGCATGCCATGATATACGA
 GGAAAGGGGACATCCCATATTCATATGTCCAGTGTCTGGGGAT**TGA**GACAGAGAAGACCCCTG
 CTTAAAGGGCCCCACACCAAGCCAGACAGCCAAGGGAGAGTGTCCCGACAGGTGGC
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTACGCCCCCACTCTCCTTTAGGGAGC
 TGAGGTTCTTCTGCCCTGAGCCCTGCAGCAGCGGAGTCACAGCTTCCAGATGAGGGGGAT
 TGGCCTGACCCCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA
 CATTAGGTTTAGTTTGTGAAAACTCCATCCAGCTAAGCGATCTTGAACAAGTCAACCTCC
 CAGGCTCCTCATTGCTAGTCTAGTCCAGGACAGTGATTCTGCTCAGAGTGGAAGATTAAGAGA
 CAACGAATGTGAATCATGCTTGCAGGTTTGAGGGCACAGTGTGTTGCTAATGATGTGTTTTTA
 TATTATACATTTTCCACCATAAACTCTGTTTGCTTATTCACATTAATTTACTTTTCTCTA
 TACCAAAATCACCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAAGAATAAAGAG
 GAGGTAGGATTTTTCTAGTATTCTATAAGCCAGCATTACCTGATACCAAAACAGGCAAAG
 AAAACAGAAGAAGAGGAAAGAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTTTAAACAAATTAACATAAACAATATTTAAAGATGATATATAACTACT
 CAGTGTGGTTTGTCCCAAAATGCAGAGTTGGTTTAATATTTAAATATCAACCAGTGTAAAT
 CAGCACATTAATAAAGTAAAAAAGAAAACCATAAAAA

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FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop .
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC
GVVMGMIIVFFKSKGKIQAELDWRKHGQAEIRDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLTLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAAGAGTTTGTGGGAACCCCTGGGTTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTCAATTATGTGAGATATAATCAAAAGAAGACCTACAA
 TTACTATAGCACATTGTCATTTACAAC TGACAAACTATATGCTGAGTTTGGCAGAGAGGCTT
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGA AAAATGCATTTTATAAA
 TCTCCATTAAAGGAAGAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG
 AGTGTGGCTCATATGCTGTTGATTTGTAGATTTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAATTTGTTCAACTTGTTTTACATGAAAAGCTGCAAGATGCTGTAGGACCCCTAAAGTA
 GATCCTCACTCAGTTAAATTA AAAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCTGCACTGGGATGGGAGTCATCGCTGT
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGTCTGCTCACTGTTTTACAACATATAA
 GAACCTGCCAGATGGACTGCTTCCTTTGGAGTAACAATAAAACCTTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAAACACCCATCACATGACTATGATATTTCT
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTTGTCTCCCTGA
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGAGCTACAACCT
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT
 AGAAGGAAAAACAGATGCATGCCAGGGTGACTCTGGAGGACCCTGGTTAGTTCAGATGCTA
 GAGATATCTGGTACCTTGTCTGGAATAGTGAGCTGGGGAGATGAATGTGCGAAACCCAACAG
 CCTGGTGTTTATACTAGAGTTACGGCCTTGCGGACTGGATTACTTCAAAAACCTGGTATCTA
 AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTGTGTTTTTGGGTGTGGAGGCCATT
 TTTAGAGATACAGAATTGGAGAAGACTTGC AAAACAGCTAGATTGACTGATCTCAATAAAC
 TGTTTGCTTGATGCATGTATTTTCTCCAGCTCTGTTCCGCACGTAAAGCATCTCTGCTTCTG
 CCAGATCAACTCTGTCTCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCA TTGTTCTCTAGAAGTTTTGTGCAATTTTGAC
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTC
 AGCTCCTCTCATTTTCAGCAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAGTATTAGGTGTTTTTCTTAGT
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC
 ACTTCATCATTTAGGAAGTATGGGAACTAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA
 TCCTTATTTTCATTTCCAACAAC TACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG
 ACCTATAATAATTATACAAACTT CATGCAATGTACTTGTCTAAGCAAATTAAGCAAATAT
 TTATTTAACATTGT TACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

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FIGURE 150

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871

><subunit 1 of 1, 423 aa, 1 stop

><MW: 47696, pI: 8.96, NX(S/T): 3

MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLEEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVYPYNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWIYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKGTI

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAAGCTTCAGCCAAACGGCATTGAAGTTGAAGATACAACTGACAGCA
CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTGAGCTGGTGGATTCCCG
CTGCATCAAGGCCTACCCACTGTCTCCATGCTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC
CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCTCAAGACTTTGAAGAAGAGGAGG
CAGATGAGACTGAGACGGCGTGGCCGCCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC
CGACACCTGCAAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCCTGCCTGTGCC
AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG
CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTCCACTACTGG
CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCGCTGAACGCTACGGTCCG
CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCGTTTGCCTAGTGGCCGCTA
ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC
CCTGCCTTCGGGCCTTGCGCCGCTTGCGGTGCCGCCCAACCCCGCACTCTGGTCCACGC
GGCCGTCGGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT
GCCTGCGCGATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCTCTGA
AAGGGGCTGGGGGCATCTCGGGCACAGACAGCCCCACCTGGGGCGCTCAGCCTGGCCCCG
GGAAAGAGGAAAACCCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG
GCTCCAGGGCCACGGCGGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT
GGCGCTTTGTTTCTGGCTGAGGTCTGGGAAGGAATAGAAGGGGCCCAATTTTTTTTTTA
AGCGGCCAGATAATAAATAATGTAACCTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

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FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEEADDETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPGLSSPAQPPDPMPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLWDGSEA
AQKGPPLNATVRRRELKGLKPGGIYVVCVVAANEAGASRVQAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAHAVGVGTALALLSCAALVWHFCLRDRWGCPRRAAARAAGAL
```

Important features of the protein:**Signal peptide:**

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCCGATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACCAGGG
 CCCAGCGCGGACGATCGCTGCCGTTTTGCCCTTGGGAGTAGGATGTGGTGAAAGGATGGGGC
 TTCTCCCTTACGGGGCTCACAATGCCAGAGAAGATTCCGTGAAGTGTCTGCCGTGCCGTGCT
 CTACGCCCTCAATCTGCTCTTTTGGTAAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTTAACTGCAGAAACGAGGGGTAGAGGAAGCAGTC
 ATTTTGACTTACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGGCTGTTTCTTATCAT
 TTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAATCTGTTGCTTCTTGATGGTACT
 TTGGAAGTTTGCTTGTCAATTTCTGTGTAGAAGTGGCTTGTGGCGTTGGACATATGAACAG
 GAACTTATGGTTCCAGTACAATGGTTCAGATATGGTCACTTTGAAAGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAT
 GCTGTGGAGTAGTATATTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCCAGAT
 TCCTGCTGTGTAGAGAATTTCCAGGATGTTCCAAACAGGCCCCACAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTTATTCCTTTTGGAGAGAACCAAAACAGTGC
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGGTGACACAAATCCTGGCCATGATTCTCACC
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGGAGCCTGGGACAGACCAATGATGTC
 CTTGAAGAATGACAACCTCTCAGCACCTGTCTATGTCCTCAGTAGAACTGTGAAACCAAGCC
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG
 GAGTTATAAAGAAAATGTACAGAGAAGAAACCAAACTGTTTATTGGACTTGTGAATT
 TTTGAGTACATACTATGTGTTTCAGAAAATATGTAGAAATAAAATGTTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAAGTTTCATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCAGTGTGTAGC
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTGAGGCAGCATGGTTTGATTAGCATTTT
 CGCATCCATGCAACAGAGTCACATATGGTGGGACTGGAGCCATAGTAAGGGTTGATTACTT
 CTACCAACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTTATTACTCAGCGATCTATTCTCTGTATGCTAAATAAATATATATCAGAAAACCTTC
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAATATTCTACCCTTAAAA
 GAGCAAGCTAACACATTGTCTTAAAGCTGATCAGGGATTTTTTGATATATAAGTCTGTGTAAA
 TCTGTATAATTAGTCGATTTTCACTTCTGATAATGTTAAGAATAACCATTAAGAAAAGGAAA
 ATTTGTCTGTATAGCATCATTTATTTTAGCCTTTCCTGTTAATAAAGCTTTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATACTTAACCACTAATTTTGAATAATTA
 CCAGTGTGATACATAGAAGATCATTTATTCAGAAATGTAGTGGTCTTTAGGAAGATTATTAATA
 GAAAATTTGCACATAACTTAGTTGATTCAGAAAGGACTTGTATGCTGTTTTCTCCCAAAATG
 AAGACTCTTTTTGACACTAAACACTTTTTAAAAAGCTTATCTTGGCTTCTCCAAACAGAA
 GCAATAGTCTCCAAGTCAATATAAATTTACAGAAAATAGTGTCTTTTTCTCCAGAAAAAT
 GCTTGTGAGAATCAATTAACATGTGCAATTTAGAGATTCTTTGTTTATTTTCACTGATTA
 ATATACTGTGGCAAAATACACAGATTATTAATTTTTTACAGAGATAGTATATTTATTT
 GAAATGGGAAAAGTGCATTTTACTGTATTTGTGTATTTGTGTTTATTTCTCAGAAATATGAA
 AGAAAATTAATGTTGCTCAATAAATATTTTCTAGAGAGTAA

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FIGURE 154

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTILTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLAWYFGSLLVIFCVELACGVWITYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCCTGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGACCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAGACCGGGAGGATCACAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGCCTCGATGTCAAACCCCTGCGCAAAACCCGATATCCCCATGGAGACCTTCAGAAAGGTGGGGATCCCCATCATATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTGTCTCATCAAGGTGATTCTGGATAAATACTACTTCTCTGCGGGCAGCCTCTCCACTTCATCCCAGGAAGCAGCTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTTCCCCGAAGGGCCTGCAGTGGCAGTCCGCCCTCTCCAAGGACCGATCCCACTGCAGGTGCTGGACTCGGCCACAGGGAACCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAGACGCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA TGTTGTTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCTCTCAGGCTCCCTGGTCTCCCTGCAGTGTCTTGCCCTGTGGGAAGAGCCTGAAGACCCCCCGTGTGGTGGGTGGGGAGGAGCCCTCTGTGGATTCTTGCCCTTGCGAGGTGAGCATCCAGTACGACAAACAGCAGCTGTGTGGAGGGAGCATCTGGACCCCCACTGGGTCTCACGGCAGCCCCACTGCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGCAGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAAAGACAATGACATCGCCCTCATGAAGCTGCAGTTCCCACTCACTTCTCAGGCACAGTCAGGCCATCTGTCTGCCCCCTTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGCTCTGACATACTGCTGCAGGCGCTAGTCCA GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA TGATGTGTGCAGGCATCCCCGAAGGGGTGTGGACACCTGCCAGGCTGACAGTGGTGGGCCCTCTGATGTACCAATCTGACCAAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG GGGCCCGAGCACCCAGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTTGCAGTGCTGGGAGCCGCTTCCTTCTCTG CCGTGCCCACTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCCCTGGGTACACCC CTCTGCCCACAGCCTCAGCATTCTCTTGAGCAGCAAAGGGCTCAATTCTGTAAAGAGACCC TCGCAGCCCAGAGCGCCCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGCTCCC AGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA GGAACCTTCCCACTACTGAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG CTGGAGAGGAGAAGGAAAGGGTCTGCGCCAGCCCTGTCCGTCTTCACCCATCCCCAAGCCTA CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT ACCTACTGTTGTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT CTGGCAAAAAAAAAA

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FIGURE 156

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSQPLNSLDVKPLRKPRIPMETFRKVGIPIIIIALLSLASIIIVVVLIKVILDKYYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPEGPAVAVRLSKDRSTLQVLD SATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDL DVVEITENSQELMRNSSG PCLSGSLVSL
HCLACGKSLKT PRVVGGEEASVDSWPWQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV
FNWKVRAGSDKLG SFPSLAVAKIIIIIEFNPMYPKDN DIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWII GWGFTKQNGGKMSDILLQASVQVIDSTR CNAD DAYQGEVTEKMM CAGIPE
GGVDTCQGD SGGPLMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWK AEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGCTGAGGCACTGAGAGACCGGAAGCCTGGCATTCCAGAGGGAGGAAACGACAGCGCATCCCCAGGCTCCAG
 AGCTCCTCGGTGACAGTCTGTGCTGAGCATGGCCCTCCCAGCCCTGGGCCCTGGACCCTGGAGCCTCCTGGGCC
 TTTTCCTCTTCCAACCTGCTTCAGCTGCTGCTGCCGACGACGACCGCGGGGGAGGGGGCAGGGGCCATGCCCA
 GGGTCAGACTATGACAGGGGATGAACGTAGGGCACTTAGCTTCTTCCACCAGAGGGCCCTCAGGATTTTGACA
 CTCTGCTCCTGAGTGGTGATGGAAATACCTCTACGTGGGGCTCGAAGAGCAATCTGGCCCTTGATATTCAGG
 ATCCAGGGTCCCCAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCCTTTA
 AGAAGAAGAGCAATGAGACAGTGTTCACACTTCATCCGTGCTCGTGGTTCTTACAAATGTACCCATCTCTACA
 CTTGGGCCACCTTCGCCCTTCAGCCCTGCTTGTACCTTCATTGAACCTTCAAGATTCTACCTGTGGCCATCTCGG
 AGGACAAGGCTCATGGAGCAAAAGCCCAAGGCCCTTTGACCCGCTCACAAGCATACGAGCTGTCTTGATGGATG
 GGATGCTCTATTCTGGTACTATGAACAACTTCTGGGCGAGTGAGCCATCTGATGCGCACACTGGGATCCCAGC
 CTGTCTCAAGACCGACAACCTTCTCCGCTGGCTGCATCATGACGCTCCTTTTGGCAGCCATCCCTTCGACCC
 AGGTGCTCTACTTCTTCTCGAGGAGACGCCAGCGAGTTGACTTCTTTGAGAGGCTCCACACATCGCGGGTGG
 CTAGAGTCTGCAAGAATGACGTGGCGCGCAAAAGCTGCTGCAAGAAGAGTTGAGCACCTTCCGAGAGGCCAGC
 TGCTCTGCACCAGCCGGGGCAGCTGCCCTTCAACGTCTATCCGCCACGCGGTCTGCTCCCGCCGATTCTCCCA
 CAGCTCCCCACATCTAGCAGCTTTCACCTCCCAGTGGCAGGTTGGCGGGACAGGAGCTCTGCGGTTTGTGCT
 TCTCTCTTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAAGAGTTGAACAAAGAACTTCACGCTGGACATA
 CTTATATGGGCCCTGAGACCACTGCGTGGCGCGCAAAAGCTGCTCAGTGGGCCCTCTCTGATAGGCGCTGAGCT
 TCATGAAGGACCACTTCTGATGGATGAGCAAGTGTGGGGACGCCCTGCTGGTGAAATCTGGCGTGGAGTATA
 CACGGCTTGCACTGGAGACAGCCAGGGCCTTGATGGGCACAGCCATCTTGTCTATGCTGGGAACCAACACAG
 GGTCGCTCCCAAGGCTGTGGTAAGTGGGGACAGCAGTGCTCATCTGGTGAAGAGATTACAGCTGTTCCTGACC
 CTGAAGCTTTGCAAACTGCACTGCGTGGCCCAACCCAGGCTGCAAGTTTGTAGGCTGAGGCTGTCTGGGA
 GGGTGCCCGAGCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCCGGAGCCCCACTGTGCT
 GGGACCTGAGTCCCAACCTGTTGCTCCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCCATGAGCAGGAGCCTTCGGCCTCAGAGCCGCCCGCAATCTATT
 AAGAAGTCTGGCTGTCCCCAACCTCATCTTGGAGCTCCCTTGCCTCCCACTGAGCTTGGCCTTCTTATT
 GGAGTCATGGCCAGCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGGCTCCCTTGTGTGATAGTGCAGG
 ATGGAGTTGGGGTCTCTACAGTGTGGGCAACTGAGAATGGCTTTTCATACCTGTGATCTCCTACTGGGTGG
 ACAGCCAGGACCAAGCCCTGGCCCTGGATCCTGAACCTGGCAGGCATCCCCCGGGGAGCATGTGAAGGTCCCGTTGA
 CCAGGTCAGTGGTGGGGCCGCCCTGGCTGCCAGCAGTCTTACTGGCCCACTTTGTCACATGATGACACATCAGGAGGTG
 TTGCTTGTAGTCTTTGAGGAGCCCTCATCATCTCGTGGCTCCCCATTGAGAGCACTCGGGGTGGGGGCAAGG
 TTCAGGGCTGTGAGACCCTGCGCCCTGGGGAGAAGGCCCGTTAAGCAGAGAGCAACACCTCCAGCTCTCCCAAGG
 AATGCAGGACCTTGCCAGTGATGTGGACGCTGACAAACACTGCTTAGGCACTGAGGTAGCTTAAACTTAGGCA
 CAGGCCGGGGTGGCGTGCAGGCACCTGGCCATGCTGGCTGGGCGGCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGCTACTCTGCACTACATGATGACACATCAGGAGGTG
 ATGCACAGCAGTCTGCCTCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTAC
 CCCAGACCTGCTCTTACATGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGAGCCCTC
 CAGAACACAGTGTTCAGAGACCCCTAAAAAACCTGCTGTCCCAGGACCCTATGTTAATGAACACCAACATC
 TAAACAATCATATGCTAACATGCCCACTCTGGAACCTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCT
 TCTCCAGGGTCATGAGGAGTGTGCTCCCTCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCAGGAAGTC
 TTTCTGAAGTCTGACCACCTTCTTCTTGTCTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGATGG
 CAGGGGTAATCTGAGCCTTCTTACTCCTTTACCTAGCTGACCCCTTCACTCTCCCCCTCCCTTTCTCTTGT
 TTTGGGATTACAAAACCTGCTGTGACAGACTGTTTATTTTATTAAAAATAAAGCTTTAAAAAA

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FIGURE 158

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGPMPRVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLNMIWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAAKHHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDSFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFMDQVVGTPLLVKSGVEYTRLAVETAQGLDGSHSLVM
YLGTTTGLSHKAVVSGDSSAHLVEEIQLFPDPEPVNRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPESTRCCLLSAPNLNSWKQDMERGNPEWACASGPMRSRLRP
QSRPQI I KEVLAVPNSILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVL FALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVADANNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAAG
 TGAGC**AT**GGCTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCCCTTCCCTGGGGTCTCGCTC
 TCAGAGGCTGCCAAATCTCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTACCATTGCTTAACCCACAAAGAG
 GTCCCTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAGAGAATTTAAAAAGAGTTTGGATTCTTCTGGAAGAACTTTAGG
 TGGCAGAGGAAAAATTTGAAAACTTATTAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTTAATAGAAAGGATATCATGGATTCCCTTAAAGAAATGAGAAGCTTCGACATGGTGATA
 GTTGAAGCTTTTGACTACTGTCTTTCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC
 CATTCTTCCACTTCATTCCGGCTCTTTGGAATTTGGGCTACCAATCCCCTTGTCTTATGTTT
 CAGTATCCGTTCTTGCTGACTGATCACATGGACTTCTGGGGCCGAGTGAAGAATTTTCTG
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTGTGACAAACCCATCAA
 GGAACATTTACAGAGAGGCTCTAGGCCAGTTTGTCTCATCTTCTACTGAAAGCAGAGTTGT
 GGTTCATTAACCTGACTTTGGCTTTGATTTTGTCTGACCTCTGCTTCCCAACACTGTTTAT
 GTTGGAGGCTTGATGGAAGAAACCTATTAAACCAAGTACCACAAGACTTGGAGAAGCTTCAATGC
 CAAGTTTGGGCTCTGGTTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGCAG
 ATCCGGAATCTTCAAGGAGATGAACAATGCTCTTGTCTCACCTACCCCAAGGGGTGATATGG
 AAGTGTCAAGTTCTCATTGGGCCCCAAGATGTCCACCTGGCTGCAAAATGTGAAATTTGGA
 CTGGCTTCCCTCAGAGTGACCTCTGGCTCACCCAAGCATCCGTTGTTGTACCCACAGGCG
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGGATCCCTCTCTTT
 GGAGCAAGCTGAAAAAGTGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTTCTATTACAGTT
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGCGGCGAGTGCTGCCAGTGTATCCTGCGCTCCCAACCCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGCGCGCAGCCATCAAGCCCTA
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTGAGAGTTTTTGTGTTTCTGCTGGGGC
 TCACCTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACAT**TAA**GGCCAGGTGCAGCCTTGGCGGGGTCTGTTTGGTGG
 GCGATGTACCACTTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCCCTT
 TAGTTATCTCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTCCACTTGC
 TAATTTTGTCTACAAATTCATCCTTACTAGCTCCTGCTGCTAGCAGAAATCTTTCAGTCTCT
 CTTGTCTCTCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTCTGAGTGACTTG
 GACCATGACCCCTCAGATTTCCAGCCTTAAATCCACCTTCTCTCATGCGGCTCTCCGAA
 TCACACCCCTGACTCTTCCAGCCTCCATGTCCAGACCTTAGTCAGGCTCTCTCACTCTCTGCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCATATTTCTTCAGTTTCTGTTT
 TGTCTCCACATATTCTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTACAGGGC
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCCTGTCTCTGGTGCCACAGTGAGCTCTCT
 TCTTGGCTGAGAGGCTGAGAGCTTAGGTTTCCAGATTTCTGAAATAATAAAGTTTACA
 GCGTTATCTCTCCCCAACCTCACTAA

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FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169

><subunit 1 of 1, 523 aa, 1 stop

><MW: 59581, pI: 8.68, NX(S/T): 1

MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHHRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLGPFFVAILSTSFGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLKAELEWF
INSDFAFDFAFPLLPNTVYVGGLEMEKPIKVPVQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVWKCQCSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPFLFGDQPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTTGGATHLKPVVFQQPWHEQYLFDFVFVFLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTTGTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTTCTGTCACACCCGTACACACACATACCATGTT
 CTCCATCCCCCAGGTCACGCCCTCAGTGCTGCCATCCAGCAGGGCTACCCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGGCAGGCGGCTTCATCCCTCCTTTCTCTCCAAAGGCCA
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTCAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAAGAGGGGCAGA
 AGACCGGGGCACTTGTGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC
 GGGTGGGCCCAGGAGGGGTCAGAGCCCGTCTGCTGGAGGGGAGTGCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGCCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC
 GAGTGGCATTGTCTGCGGTCGGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC
 ACCAGTGGGGCCATCTACTTCGACCAGGTCTGGTGAACGAGGGCGGTGGCTTTGACCGGGC
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGCTACAGCTTCCGGTTCCATGTGGTGAAGG
 TGTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTATCTAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCAGCTGTGTGCTACTGCCCTTGGG
 CCCTGGGGACCGAGTGTCTCTGCGCTGCGTCCGGGGAATCTACTGGGTGGTTGGAAATACT
 CAAGTTTCTCTGGCTTCTCATCTTCCCTCTCTGAGGACCCAAGTCTTTCAAGCACAAGAAT
 CCAGCCCCGACAACCTTTCTTCTGCCCTCTCTTGCCCCAGAAACAGCAGAGGCAGGAGAGAG
 ACTCCTCTGGCTCCTATCCCACCTCTTTGATGGGACCCCTGTGCCAAACACCCAAGTTAA
 GAGAAGAGTAGAGTCTGGCATCTCCAGACAGGCCTTCCACCCACCCACCCACAGTTACC
 CTCCAGCCACCTGCTGCATCTGTTCTGCTGCGCTGACGCCCTAGGATCAGGGCAAGGTTGGCA
 AGAAGGAAGATCTGCATCTTTGCGGCCCTGCTCCTCCGGTTCCCCCACCAGCTTCCCT
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCCCACAGGAGGCCAG
 ATGGACAAGCCTCAGCGTACCTGTCAGGCTTCTTCTGTGAGGAAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCCGTATGGCTAGGGTGGGAGGCTCAGCCAC
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTTGTCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTTGTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCATCCTCTTGCTTGGCCACCTCCTGAACTGCTCCAC
 CTTTGAAGTTTGAACCTTTAGTCCCTCCACACTCTGACTGCTGCCCTCCTTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCAGCATATCCCCACTATCTCTCTTCTCCTGAT
 CTGTGCTGTCTTATTTCTCTCCTTAGGCTTCTATTACCTGGGATTCATGATTCTATCCTT
 CAGACCCTCTCTGCCAGTATGCTAAACCTCCCTCTCTCTTTCTTATCCCGCTGTCCATT
 GGCCAGCCTGGATGAATCTATCAATAAAACAACTAGAGAATGGTGGTCAGTGAGACATAT
 AGAATTACTAAGGAGAAGATGCCCTGGAGTTTGGATCGGGTGTACAGGTACAAGTAGGTA
 TGTGTCAGAGGAAAATAAATATCAAACGTATATACTAAAATTAATAA

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FIGURE 162

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180

><subunit 1 of 1, 205 aa, 1 stop

><MW: 21521, pI: 7.07, NX(S/T): 1

MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLLEGECVVCPEPGRAAAGGP
 ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
 SFRFHVVKVYNRQTVQVSLMLNTWPVISAFANDPDVTREATSSVLLPLDPGDRVSLRLRRG
 NLLGGWKYSSFSGFLIFPL

Signal peptide:

amino acids 1-32

[illegible]

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop .
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIHAVLYFTWLVDWNTPKKGRRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLRREYLMMSGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSSM
PGKNAVTLNRNKGFKLALRHGADLVPIYSFGENEVYKQVIFEEGSGWRWVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYEALVKLFDK
HKTKFGLPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

[illegible]

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FIGURE 166

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVVFVSGLVINLVQLCTLALWVPVSKQLYRRRLNCR LAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTNLNFRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRRRLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTTATTTTAAAGAACTGAAGTACTATGCATCACTCCCTCCAATGTCCTGGGGCA
GCCACCAGGCATATTTCATCTTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT
GCTTATTTCTTTGGTAGGAAAGGGCTCAGTTTGTCTTGTGGGGTTGGTGGCAGGCAGGCCG
GCTTACGCCTGATACGGCCCTGGGTTAGAAGGGAAGGGAAGATAAACTTTTATACAAATGGG
GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT
TTCTCTAACCTGGCATACCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTCTTAGGATCAA
AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCCCTGGCCAGCTTCATGT
ACATGTGGTGTCTCTTGTCTGCTTCCTGTAATGTGGTATGCCATGGGGTCTTTGCACAAGCCT
TTCTCTTTTGGCTGGACACTGTTCCCTGCCCCCCCCATACTCTTCCTACTTAATATGTAGTC
ATCCTGCAGATTTCAATTCTAACATCATTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT
CTTGTTTAAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCACTTGGCACTCAGTTGTA
TCTTTATGTGCGTTTGTGGTTGTATGGGTTGTGTCTGTTCCCAAGATGCCAGCTCTGAGC
TGCGTGAGGGTCAAGGGCATTGCTGTGCCTGCCAGGTATAGTGCCCTACATGTGGTGGGTGCT
CATGTTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAGTTCACCA
GATGGTGTAGGGCCCAGCATTGTAAATTCACACGTTGACTGTGCTTGTGAATTATCTGGGGA
TGCAGGTCCTGATTAGTAGGCCAGGTTGGGCATCTCTAACAACTCCCACGTGATGCTGA
TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGGC
TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT
TCAAGACTAGCCTGGCCACATGGTGGAACCCATCTGTACTAAAAATACACAAATTAGCTG
GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG
AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACCGGGTGAC
AGAGTGAGACTCTATGTCCAAAAA

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FIGURE 168

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHHLCVCFSFALALGHFLLISLVGKGLSLSCGVGGRQAGRLRLRPWVRR
EGKINFYFTNGDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC
 AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCTACTCTACCTAC
 ATTAATACTGTCTTTTGTCTCTTGTAACTAGCCTTTACCTTCCTAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGCACCTGACTCGGGCAGTGAGGTAGCTGAGCCTCTTGGTA
 GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGCAAGCCCGAAGATTT
 CATAGGCGATGGCTCCCACTGCCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT
 CTAACCTTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGCACTTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGCCA
 GGGGAAGGAACCTTGTGCCAAATTATGGGTGAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTTCAGTGGACATGTGGGGGAAGGGGTGCCGATGGCGCATGACACACT
 CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCCGCCCGATCCACGTACCAGTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG
 CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCCTCCTTCCCCTC
 TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG
 GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCCAGGCAAGGACTGTGTGGCT
 CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTGTAATTTGAAACCCCAAG
 TCCAAACCTAAGAACCAGGTGCATTAAGAATCAGTTATTGCCGGGTGGGTGGCCTGTAATG
 CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAAGCCTG
 GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGTGAGACAGGAGAACTACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAGAATTATGGTTATTTGTAA

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FIGURE 170

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
```

Signal peptide:

amino acids 1-15

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FIGURE 171

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCCGCGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCCCGCGCGCT
 GGCCCTGGGCTCAGCCGCACTGGGCGCGCCTTCGCCACTGGCCTCTTCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTTCCCCCGAGGACAGCCGCCTGTGG
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC
 CCTGGAGCAGCCGAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTCTTGGCCAACC
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGCACCTTCACGGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCGCGGACGGGCGCGTGGTGACCTGCGAGGTGGACGCGCA
 GCCCCGGAGCTGGGACGGCCCTGTGGAGGCAGGCCGAGGCGGAGCACAAAGATCGACCTCC
 GGCTGAAGCCCGCCTTGAGACCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC
 AACCTCCGAAAGGGGACGTGGCGGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGACTCACCTTGGCCTTCAAGAT
 CTAGGGCTGGCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC
 CCTGAGTTTAAATTCGAAAATAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

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FIGURE 172

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSR
MREHPALRSLRLLTLEQPQGDMMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALAL
PADGRVVTCEVDAQFPELGRPLWRQAEAEHKIDRLKPAETLDELLAAGEAGTFDVAVVDA
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI

Important features of the protein:**Signal peptide:**

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

CCGCCGCCGACGCCGTACCGCCGCTGACAGCGCTTTCGCGGCCTGGCGCTCTCGCCGTCAG
G**TG**CGCCACACGCCCTTCAAGCCCGGGAGCTTGGTGTTCGCTAAGATGAAGGCGTACCTCCAC
TGCCCTGCCAGGATCGACGACATCGCGGATGGCGCGTAGAGCCCCCAACCAAGTATCCC
CATCTTTTTTCTTTGGCACACAGAAACAGCCTTCTCTGGGACCAAGGACCTGTTCCCTTACG
ACAAATGTAAAGACAAGTACGGGAAGGCCCAACAGAGGAAGAAAGGCTTCAATGAAGGGGTGTGG
GAGATCGAGAACACCCCCACGCCAGTACAGCGCCCTTCGCCAGTGAAGCTCTCCAGACG
CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTACGCTGACGAGAGCAGTATGAGGACCGG
GGGTCTAGGCCCTCACAGCGTATACGCCACAGCTGCCAGCGACAGGATGGAGAGCGCATCA
GACTCAGACAAGAGTAGCGACAACAGTGGCCTGAAGAGGAAGACGCTGCCGTAAGATGTCT
GGTCTCGAAGACGAGCCGAAGGCGCTTCAGCGCTTGAAGCTGGATCAGGCCAGCGTGTCCCATCCG
AAGAGGAAACTCGGAAGCTCATCTGAGTCGGAGAAGACCGGACGCCAGGACTTACACCT
GAGAAGAAAGCAGCGGCTCCGGGCGCCACGGGAGGGGCCCTCTGGGGGACGGAATAAAAGAA
GGCGCGCTCAGCCTCCGACTCCGACTCAAGCGCGATTTCGAGCAGGGGCAAGCTTGAGCGG
TGGCATGGCGCGGTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCCGACTCCGATGTG
TCTGTGAAGAAGCTCCGAGGGGACGAGGACCGACGGGAGAAGGCTCTCCGGAAGCCGCGAGG
CGGAAACAGAGCCTGAACGGCTCTCGCTCAGCTCAGAGTACAGTACAGCGACGAGG
TGGACCGCATCAGTGAAGCGGCGGGACGAGGCGCGGAGGCGGAGCTGGAGGCCGCGG
CGCGCGGAGAGCAGGAGGAGGAGCTGCGGCGCTTCGGGAGCAGGAGAAGGAGGAGAAGG
CGGAGGCGGACGCGGCGCCAGCCGGGGAGGCTGAGCGGGGACGCGGCGGACGCGGCGG
ACGAGCTCAGGAGGAGCAGTACAGCCGCTAAGAAAGCGGGGACGAGGCCGCGGCGGGGT
CCCCGCTCTCTCTCAGTCCGAGCCCGAGGCCGAGCTGGAGAGAGGCCAAGAAATCAG
GAAGAAGCCGAGTCTCAAGCACAGAGCCCGCAGGAACTGGCCAGAGGAGAAGAGAG
TGGCGCCGAGGAGAACCAACAGGACCGCTGAAGGTGGAGCGGACCCGGAAGCGGTCC
GAGGCTCTCGATGACAGGAAGTAGAGAAGAAAGAGCCCTCTCGTGGAGGAGAGCT
GCAGAAGCTGCACAGTAGATCAAGTTTGCCCTAAAGTGCACAGCCCGACGTGAAGAGGT
GCTGATGCCCTAGAGGAGCTGGGAACCTGCAGGTGACCTCAGATCTCCAGAAAGAC
ACAGACGTTGGTGGCCACTTGAAGAAAGTTCCGCTTTACAAGCGCAAGGACGTAATGA
GAAGCGACGAGAAGTCTATACCCGCTCAAGTGCGGGCTCTCGGCCAAAGATTGAGCGGT
TGCAAGAGCTGAACAAGCTGGAGTGGAGAAGGAGAAGGCCAGGAGAAGTGGCCGGGAG
GAGCTTGGCGGGGAGGAGCCCCCAGGAGAAAGGCGGAGGACAAGCCAGCCAGCCGATCTCT
AGCCCCAGTGAATGGCAGGCCACATCAGAAAGGGGAGAGGCCAGGACAAGGAGGACAG
AGGAGGTTTCGGACTCGGAGAGGGGCGCAAGGTGTGGCTCTCTGAAGACTGCACGACAG
GTACGGGAGGGTCCGACCTGGACAGGCTTGGAGGACACCGGACGAGGAGCGGAGAGGCGAG
GGGGAGCTCGAGGCGCTGGACAGGAGAGCT**GA**AGCCGCGGCGAGGCCAGGCCAGCCCCCG
CCGAGCTCAGGCTGCCCTCTCTTCCCGGCTCGAGGAGAGCAGAGACGAGAACTGTGG
GACGCTGTGCTGTGTGTTATTTGTTCTTGGTTTTTTTTTCTCGCTAATTCTGTGATT
TAAACCAACATGAATGACTATAACGGTTTTTAAATGA

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FIGURE 174

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD
KCKDKYKGNKRRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDEDRG
VMAVTAVTATAASDRMESDSDSDKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE
EENSESSSESEKTSQDFTPEKKAARAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDSVKPKPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV
DRISEWKRRDEARRRRELEARRRREQEEELRRLREQEKEEKERRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKKSAKKPQSSSTEPARKPGQKEKRV
RPEEKQQAQKPVKVERTKRSEGFSDMRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVTATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV
QKVNKAGMEKEKAEELKAGEELAGEEAPQEKAEDKPSTDLAPVNGEATSQKGESAEDEKEH
EGRDSEEGPRCGSSDLDHDSVREGPDLDPRGSDRQERERARGDSEALDEES
```

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTTCACCTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATTAAATTA
 ACACCACTTTGAAGAGAACATTTGTTTCATCATGAATGCTAATAAAGATGAAAGACTTAAAGCCAGAGGCCAAGA
 TTTTCACTTTTCTGCTTTGATGATGCTAAGCATGACCATGTTGTTTCTCCAGTCACTGGCATTGGAAGCA
 AAAATATTCCAAGACTCAAGCTTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCTTTTGGGTTCACTC
 AGAAGGACTGGATTTTCAAACCTTCTCTTATAGATGAGGAAAGGCGAGGCTGCTCTTGGGAGCCAAAGACCACAT
 CTTTCTACTCAGTCTGGTTGACTTAAACAAAAATTTTAAAGAAGATTATTGGCCTGCTGCAAGAGACGGGTGGGA
 ATTTATGTAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAAATTCATCAGAGTACTCAGCCCTATAACAA
 AACTCACATATATGTGTGGAAGCTGGAGCATTTTCAATCAATATTGGGTATATTGATCTTGGAGTCTACAAAGGA
 GGATATTATATTCAAACTAGACACACATAATTGGAGTCTGGCAGACTGAAATGTCTTTCGATCTCAGCAGCC
 TTTTGCTTCAGTAATGACAGATGAGTACCTTACTCTGGAACAGCTTCTGATTTTCTTGGCAAAGATACATGCATT
 CACTCGATCCCTTGGGCCACTCATGACCACCCTACATCAGAACTTGACACTTCAGAGCACTACTGGCTCAATGG
 AGCAAAATTTATTGGAACCTTCTTCATACAGACACCTACAATCCAGATGATGATAAAATATATTCTTCTTTTCG
 TGAATCATCTCAAGAAGGAGTACCTCCGATAAAACCATCTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGT
 AGGAGGACAACGACGCTGATAAACAAGTGGACGACTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAG
 TGTGGGGCAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCACAAGAGATGAAAGAAATCCTGT
 AGTATATGGAGCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGCTGTTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGTGACAGCCATCGTTGGGTGCAGATATGGGGAAT
 TCCTTATCCACGGCTGGTACATGTCCAGCAAAACCTATGACCACCTGATTAAAGTCCACCCGAGATTTCACGA
 TGTGTCACTCAGTTTTCATAAAGCGGCAGCTGTGTGATGATAAGTCCGTATACCCAGTTGCGAGGAGCCAACTG
 CAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATGATGTCATTGCGAGAAGTGGCCGATACGA
 TGTAAATGTTTCTTGGACAGACATTGGAACCTGCTCAAAGTTGTCAGCATTTCAAAGAAAGTGGAAATAGGA
 AGAGTTAGTGGTGGAGGAGTTGCAGATATCAAGCACTCATCAATCTGTTGAACATGGAAATGTCTCTGAAGCA
 GCACAAATGTACATTTGGTTCCGAGATGGATTAGTTAGCTTCTCTTGCACAGATCGACCACTATTGGGAAGC
 TTGCGCAGACTGTTGCTTGCAGAGAGCCCTACTGTGCTGGGATGGAATGCATGCTTCGATATGCTCTTAC
 TTTCAAAGGAGAGCTAGAGCCCAAGATGAAAATATGGCAGCCCAATCACCCAGTCTGCGGACATCGAAGCAG
 CATTAGTCTATGAACTGCTGATGAAAGGTTGATTTTGGCATTGAATTTAATCTCAACCTTTCTGGAATGATACC
 TAAATCCCAACAAGCAACTATTAATGGTATATCCAGAGGTCAAGGGATGAGCATCGAGAGGATGAGGCCGA
 TGAAGAAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAGAAGAGGATCTCGGATGATATTCTG
 CAAAGCCAGGAGCACACTTTCATCCACACCATAGTGAAGCTGACTTTGAATGTCTAGATGTAGAACTGAACATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGCGAGGTCAAGGATCTATTGGCTGAGTCCGGTTGAGATACAAAGA
 CTACATCCAAATCCTTAGCAGCCCAAACCTCAGCCTCGACCACTGCGCAACAGATGTGGCACAGGGGAAAGCG
 GAGACAGAGAACAAGGGGGGCCAAAGTGAAGCACATGCAGGAAATGAAGAAAGAAAGCAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAGTTTTCTACTTAAATTAAGAAAGAAATTCCTTACC
 TATAAAAAATTTGCTTGTGTTTGTATATCCCTTATAGTAATTCATAAAATCTCCCATGGAGTTTTCGTAAAG
 CACAAGACAATAATCTGAATTAAGACAATATGTAGTAATAAGAAAGGGCAAAATTCATTTTGAACGACTTTT
 CCAAGACAATAATCTTGACACAGCAAGATATAAGAAATATCCTAAAAATAGGGGGTTACAGTTTGAATATTTT
 TGTTTTGAGTTTGGAAATTTATGTCTGTAATAGTTGAGCTAAGCAGCCCAATTTGATAGTGTATAAGCT
 GCTTTATCCCTCGAATGTCCATTAAGCATGGAATTTACCATGCAAGTTGTGCTATGTTCTTATGAACAGATATAT
 CATTCCTATTGAGAACCAAGCTACCTTTGGTAAAGGATAAGAGGTCAGACACAATTAAGACAACCTCCATATC
 AACAGGAAGCTTCTCAGTGAGCCATTACTCCTGGAGATGATATAGGAATTTGGAAGAGTGTCATTTCTTTCT
 TGCCACTGGGGTTAAATTTAGTGTACTACAACTGATTTACTGAGGCCATCATGTTTCCCCAGGATTTCT
 ATTGACTAGTCAGGAGTAACAGGTTGCAGAGAGAAGTTGGTGCTTAGTATATGTTTTTTAAAGTATATACTAA
 GCTCTACTAGACAGAAATGCTTAATAAAGCAATTTAATAAGATATGGGAATAATTTTAAATAAACAGGAACA
 TAATGATGTATAATGGCTCTGATGGGAAGCATGCAGATGGGATTTGTTAGAAGACAGAGGAACAGCAGCCAT
 AAATCTGCTGTTTGGGAAACTCATATCCCCATGAAAGGAAGAACAACTACAAATAAAGTGAGACTATGTAA
 TGGAGCTCTTTTCTAGGATATAAGTAGCTGCCAATTTGTAATTCATCTGTTTAAAAAAATCTAGATATATAA
 AACTGCTAGCAAAATCTGAGGAACAATAAATCTTCTGAAGATCATGAGAGGTAGACATTTTATTTATTAAC
 AATGATATTTCAGTATATTTTCTCTCTTTAAAAAAATATTATCATACTCTGATATATTCTTTTCTTACG
 CTTTATTCTCTGATATTTGGATTTTGTGATTATTTGAGTCAATAGGAGAAACATATATACACAGCA
 GAATTAAGAAATGACATTTCTGGGAGTGGGGATATATATTGTTGAATAACAGACGATGTAAATTTTAAAC
 AAGCGAAAGGGTAAATTAACCTTTGACATCTTCACTCAACCTTTCTCATTGCTGAGTTAATCTGTTGTAAT
 GTAGTATTGTTTTGTAATTTAACATAAATAAGCCTGCTACATGT

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FIGURE 176

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLRLKLTYSKDLLLSNSCIPFL
GSSEGLDFQTLTLLDEERGRLLLGAKDHIFLLSLVDLNKNFKKIYWPAKERVCLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRTDISEHYWLNAGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDKTIILSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSVAVCVSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVVISKEKWNMEEVLEE
LQIFKHSSIIILNMLSLLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPITQCWDIEDSISIHETADEKVIFGIEFNSTFLECIPKSQQA
TIKWYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYCKAQEHTFIHTIVKLTNLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRRNRHHRDLDELPRAVAT

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACTGAGCTGGAAGCCGAGAGGTCATCTTGAGCATGCCACC GCGGGGAGCAGA
CACCTCCCGAGTAACTGGGAGCAAGACCTGAAGCTGTTCTTCAGGAGCCTGGTGATTTTCCCCACCCAC
CTCAGAGCTTTCAGCCAGAGGGAGTATCAGGTGTGTCTCGGAGTGGGGAGCAGAAGGGCTGGCTGGCAAGA
GTGGCCTGGAGAAAGAGGTTTCAGCGCTTGACCAGCCGAGCTGCCGTGACTACAAGATCCAGAACCTGGGCATC
GGGTGAGGTGGGGGGACAGGTGTCATGTGCACCTTTCTTCTCAGCAAGAAGAGCTGAGAGAGGGGATCTTGG
AGCCATTAGGGGTGTCTAGAGCTACAGAGGGGAGGAAAGGTATTTAAAGGTAAGACTGTGGCACAATAGTTAA
GAGCAGAGTTTTTGGAGCTAGACCACATAGGTTCAAATTTCTTCTGTGTCTTCCATGTTCTGTAGCCCAAGT
AAGGGAGTGACTTAACCTCTCTGGACTCAATTTCTCATCACTAAAGTAGGGCCAAATATAGCACCCACCTCAT
AGGGAAGATTAAATGACATAATGTATGTGATGCACTCAACTAGCAAGTACCAGTCCCATAGTAAGTCATGCCACAG
TATTTCCACCCACCCCTGTTCTCTGCCTTCCCAACCAGGTAAGTCAACAGCTGGAGCAGAGGCGGAGCAGGCTT
CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGACTCCGCGGGCAGAGTGGACCC
AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTCAGGGGGCTGGCTAGATGTGGAGCGCTGGCTGAAGCCAGCAGA
TGACCCAGGCGCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGTCCCAGAGGGACCTTCTCTC
CAACCGCTGAGGATGCTGAGCTTTGACTTTGAGGAATGTAGGAGACGGGAGAGCTCTTTGAGGAGCTGGCC
CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACACGTGGTATTTCCGTATCAGGCAGGGCGTGAGATG
AGCTGACAATACGGAGGGTGAGTGGCTGGAGGTCTATAGAGGAGGAGAGTGTGACGAATGGGTCAAGGCTCGGA
ACCAGCAGCGCGAGGTAGGCTTTGTCCTGAGCGATATCTCAACTTCCCGGACCTTCCCTCCAGAGAGCAGCC
AAGACAGTGCACAACTCCCTCGCGGGCAGAGCCACAGCATCTCTGGCACAGGCCCTGTACAGCTACACCCGACAGA
GTGCACAGGAGCTGAGCTTCCCTGAGGGGGCACTCATCCGTCTGCTCGCCGGCCCAAGATGGAATAGATGACG
GCTTCTGAGGGGAGAAATTTGGGGGCGGTGTGGGGTCTTCCCTTCCCTGTGGTGGAGAGGCTGCTTGGCCGCC
CAGGGCCACCTGAACCTCTCTGAGCTGAACAGATGCTGCCGTCCCTTCTCTCTCCAGCTTCTCCCACTGTCCAC
CTACCTTGTGTGTGGATGGGCCCCCTGCACCTGTCTGCTGGGACAAAGCCCTGGACTTCCCTGGGTTCCTGG
ACATGATGGCACCTGACTCAGCGCGATGCGTCCACCACCTCCCGCCGCTTAAAGCCCCGGAATCTGTGCCAC
CAGATCCCTCACCTGAAGCCAGGGAAGCCTTGACCCCAAGTATGCTGCTGTCCCTATCTCAAGCTGTCAGA
CCACACCATCAATGATCCAGAGCAGCAGCCAAAGAGTGAATGCCCTTATTTCCACCTTCACTCCAAAGGGT
GGAACCTTGCCCTTCCCATTTCTAGAGCTGGAACCCACTCTTTTTCCTATCTATCATCTCTAGGACG
GGAACCTACTACTTCTCTTCTGTATGACCTATCTAGGGTGGTGAATGCTTAAATCTCTGGGGCTGGAACCC
ATCCATCAAGGTCTCTAGTAGTTCTTGGCCCACTCTTTCCCACTCTGGCTCCATGACCCACCCACTCTTGAATG
CCAGGGTCACTGGGGTTGGGCTGGGGAGAGGAACAGGCGCTTGGGAATCAGGAAGCTGGAGCAGATGCGAAGAC
CTGTAATGGTCTGAGCGGATTTATTGACAATGAATAAAGGGCAGCAAGGCCAGGCCAGGGCTCGGGCTCTTGTG
CTAAGAGGGCAGGGGGCTACCGTGCTATTGCTTTAGGGGCCACCCAGCGGAGGGGCTGCTGCCCTGCCAC
GCTCTATCATATGAGGAGCAGGTGTTGGGGAGGCGGGGAGGCGAGCTGTTGAGGAGGGGAGGAGGAAGAC
TGAGGGGCTGTGACTCTCTGAGGCCCCAGCTGAGACTGTGCACTCCAGGTGGAATGAGACTGTGTCCCTC
AGCTGGGGGGCAGTGCTGTCCAGTGGAGGGAGGGCTTTACGCCCAACCCACCTGGCCCTGCCAGCTGGTGA
TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAATAACACTGTGTCTCTGTCTCAAGCTGTGTCAAG
TTTTCCCTGGGGCTCAGGACCTTCCCTACCTCCACCACCAAGGGATTTATAGCAAAAGGCTTAAGCCTGCG
AGTTTACTCTGGGGTTTCAGGCGGCTTGGAGAAGAGGCTTAAATAGTTTAAGTAGGTGATGGAGATGAGATTACCTCA
TTTAGGGCTCAGGCAGACTCACCTCACATCTCCCTGCTCCCTGTGGTAGAGACCTTGAGAGAAGGGGGGGGG
TCAACAATGAGAGACCAGGATGAGTGTCTATCAGTGCCCCAGTAGTAGAGCAATAAGAGAGCCAGCCAGCTGC
AGTCCCGGCTGTGTTTTCCTACCTGGTGTACAGAAGTGTCTGGTTGCTTGGCTGCCATTTGGCTCTTGAAGTGG
GCAAGCTGGGCTTGGGCCCCCTCCCTCGGCCCTCAGTGTGGCTCTGCAAGAGCTCTGGGGTTCCTTCAAGTG
CAGAGGGGTTAGGCTGTCTGCTTGTAGTCTCCATTTCTGACTGGGGGGCTGGCTAGGACCTGGGGCTGTGGCC
TCTCAGGGGAGGCTCTCCATGGGAGCAGCTCCCTGCCTTGGGCTGCCCTCCCAAGACCCCTGACACCCCTG
GGTCTGTGTCGCCACAGAGCCCAAGCTCTGCTGTGGGGGAGCCATCAGCGTGTCTGTCAGTCCATAGGCTCT
TCTCAATGTGTCTACCCCGAAGCTTGGAGGGGAGGGAACACTGGGCTTACGACCAACTCAGAGCTGCTGCTG
GCCCTCCCTCTACACGAGGACACTCTGAGTTTGGTGGCTACTTCCCTCTGGGCTAAGGTAGGGGGAGGCTCTGT
AGATTGGGGCAGACTGTGTAGCTGACTTCTGTGGAGCTCCAGTCCAGGAGAAGAGCCCAAGGCCACTCT
TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACTGCCCACTGCGGCA
CAGAGAACCAAGTGTCTCCCTGTCCGGGGGGGCTTTTCTTCTTGGAGGCTCCCTGACGCAAGTGGAG
GGCTCTTGTGGGCTGCAATGGATGCAAGGGGCTGAGAGCCAGGCTGACTGTGTGATGATGGAGGGGGCTC
CGTCTGCGAGCTGGAGGTGGGCTCCACTGGACACTGGACAGGAGGGGATGAGGTTAACTATTCATTTCCCT
TCATGTTTTGTTTCTTACGTCTTTTACAGATGCTCTTAAACCCAGAGGCCCAATTTCCCAAGGCCCATTT
TTTCTTGTCTTTATCTAATAAATCAATATTAAAG

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FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLC LPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFYQAGREDELTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESQSDSNPCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPDGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGACAGGGCAGGCACAGAAAGCGGCCACAGAGTCTACAGAGGAGAGGGCCAGAGAAAGCTGCAGCA
 AGACACAGGCAGGGAGAGACAAAGATTCAGGAAAGGAGGGCTCAGGAGAGAGAGTTTGAGAAAGCCAGACCCCTGG
 GCACCTCTCCCAAGCCAAAGGACTAAGTTTCTCCATTTCCTTTAAACGGCTCCTCAGCCCTTCTGAAAACCTTTGCC
 TCTGACCTTGGCAGGAGTCCAAAGCCCCAGGCTACAGAGAGGAGCTTCCAAAGCTCAGGCTGTGGAGGACTTTGGT
 GCCCTAGACGGCCCTCAGTCCCTCCAGCTGCAGTACCAAGTGCATGTCCAGACAGGCTGCATCCCGGAGGGGG
 TCTGGCAGGGCCCTGGCTGTGGGAGGCCAAACCTGCCTCCTGCTCCCCATTTGCCCCTCTCTCTGGCTGGTGTG
 GCTGCTTCTGCTACTGCTGGCCCTCTCTCTGCCCTCAGCCCGGCTGGCCAGCCCTCCCGGGGAGGAGAGAT
 CGTGTTCACAGAGAGCTCAACGGCAGCGTCTGCTGGCTGGGCGCCCTGCCAGGCTGTTGTGCGCCTTGCA
 GGCTTTGGGAGAGCGTGTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGCAGGGGGCTGCAGCTGCAGTA
 CCTGGGCGAGCGCCTGAGCTGCTGGGTGGAGCAGAGCCTTGGACCTTACTGCTGGACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTGCACTGGGATGGGAGAGCCCTGTAGGCGTGTACAAATATCGGGGGCTGAATCCCA
 CCTCCAGCCCTGGAGGGAGGACCCCTAACTCTGTGGGGACCTGGGGCTACATCTACGCCGGAAGAGTCC
 TGGCAGCGCTCAAGTCCCATGTGCAACGTCAAGGCTCTCTTGGAGCCCCAGCCCCAGACCCGGAAGAGCCAA
 GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCCGATTCACAGGTGC
 GGGGCTAAAGCGCTACCTGTCAACAGTGATGGCAGCAGCAGCCAGGCGCTTCAAGCACCAAGCATCCGCAATCC
 TGTCACTTGGTGGTGACTCGGCTGATCCTGGGGTCAAGCGAGAGGGGGCCCCAAGTGGGGGCCAGTCTGTC
 CCAGACCTTGGCAGCTTCTGTGCTTGGCAGCGGGGCCCTCAACACCCCTGAGGACTCGGGCCCTGACCATCTTGA
 CACAGCATTTCTGTATTACCGCTCAGGACCTGTGTGGAGTCTCCACTTGGCAGCTCGGGTATGGCTGTGTGGG
 CACCGCTCTGATCCCGGCTCGGAGCTGTGCCATTTGTGGAGATGATGAGGCTCAGTCAAGCTTCACTGCTGCTCA
 TGAATGGGTGATGCTTCAACATGCTCCATGACAACCTCAAGCCATGATGCTTGAATGGGCCCTTTGAGCTC
 CTTCTGCCATGTATCGGCCCTGTGATGGCTCATGTGGATCTCGAGGAGCCCTGTGCCCCCTGCATGCTCCCGCT
 CATCACTGACTTCTCGACAGTATGGTATGGGCACTGTCTTAGACAACCCAGAGCTCATCTGCATCTCGCTGTG
 GACTTTCCCTGGCAAGGACTATGATGCTGACCGCCAGTGCCAGCTGACCTTCCGGGCCGAGCTCAGCGCATTTGTCC
 ACAGCTGCGCGCCCTGTCTGCCCTTGTGCTTGGCCACTGAGGCTCAAGCTTGGCCGCGATGTGCCGGAAGACCA
 CTCGCCCTGGGCGGATGGCACACCCCTGCGGGCCCGCACAGGCTGCATGGTGGTGGCTGCCCTCCATAGGACCA
 GCTCCAGGACTTCAATATTTCCACAGGCTGGTGGCTGGGGTCTTGGGACCATGGGTGACTGCTCTCGAGACT
 TGGGGTGGTGTCCAGTTCTCTCCGAGACTGCACGAGGCTGTCCCCCGAATGGTGGCAAGTACTGTGAGGG
 CGCCGCTAGCCGCTTCCGCTCTGCAAACTGAGGACTGCCCACTGGCTCAGCTCAGCTTCCGCGAGGAGCA
 GTGTGCTGCTACAAACACCGCACCGACCTCTCAAGAGCTTCCAGGGGCCATGAGCTGGGTCTCTCGCTACAC
 AGGCTGGGCCCCCAGGACAGTGAACCTACGCTGCCAGGCCCGGCTGAGCTACTACTATGTGCTGAGAGCC
 ACGGCTGGTAGATGGGACCCCTGTTCGCCGAGACGCTCCTCGGTCTGTGTCAGGCGCGATGATCCATGCTGTG
 CTGTGATCGCATATTGGCTCCAAGAAGAAGTTTGACAAGTGCATGGTGTGCGGAGGGGACGGTTCTGGTGTGAG
 CAAGCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATACAAACATTTGGTCACTATCTCCCGCGGGGCCACCCA
 CATTCTTGTGCGGACAGGAAACCTTGGCCACCGGAGCATCTACTTGGGCTGAAGCTGCGATGGCTCTTA
 TGGCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTATGCTGCTGGGCGAGCTGCTGCGCTTA
 CAGCGGGGCCACTGCAGCCTCAGAGCACTGTCAAGCCTTGGGCACTGCGCCAGCTTGAACACTGCAAGTCTCT
 AGTGGCTGGCAACCCAGGACACACGCTCCGATACAGCTTCTCTGCTGCCCGGCCGACCCCTTCAAGCGCAG
 CCCCCTCCCAAGGACTGGCTGCACCAAGAGCACAGATTCTGGAGATCTCTCGCGCGCCCTGGGCGGGCAG
 GAAATTAACCTCACTATCCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTTACTCGGGAGAAAGAGAGAGCTT
 CTGCTGCTGCTCATGTAAAGCTCAGTGGGAGGGGCTGTGGGCTGAGACCTGCCCTCTCTCTGCTCTCAAT
 GCGCAGGCTGCTCCTGCCCTGGTTCTCTGCCCTGGGAGCAGTATGGGTACTGGCTGGAAGGGGCTGACAGAC
 AGCCCTCGCATCAACTGACCCCTGCTGCCCTCGGGTCAAGAGGAGGGGAGGAGCAGGGAGGGCTCGGGGCC
 CAGTTGTATTTATTAGTATTTATTTACTTTTATAGCACAGGGAAGGGACAAAGCACTAGGGCTCTGGGGAA
 CTTGACCTTCAACCTATAGCCCTCAACCTGGGCTAGGAAATCAAGGTAGGGTGGGCTCAGGAGGTGAGGGATTTCTTT
 TGTGTATGCGTGTGTGTGTGTGTGAAATGTGTGTGCTTATGTATGAGCTCAACCTGTGTCTGCTTCTCTCT
 TCTCTGAATTTTATTTTGGGAAAGAAAGTCAAGGTAGGGTGGGCTCAGGAGGTGAGGGATTTATCTTTT
 TTTTCTTTCTTTCTTTCTTTCTTTTCTTTTGTAGACAGAACTCTGCTCTGCTGCCAGGCTGGAGTGCAATG
 GCACATCTCGGCTCACTGACTCTCCGCTCCCGCTCCGGGTTCAAGTATTTCTCATGCTCAGGCTCGAGTGTGAGTGTG
 GGATACAGGCTCTGCCACACGCCAGCTAATTTTGTGTTGTTTGTGGAGACAGCTCTGCTGCTGAGTGTG
 ACCAGGGCTGGAATGATTTCACTCACTGCAACCTTCGCCACCTGGGTTGAGCAATCTCTGCTGCTCAGGCTCC
 CGAGTAGCTGAGATTTATAGGCACCTACCACACCGCCGCTAATTTTGTGTTTGTGGAGACAGCTCTGCTGCTCAGGCTCC
 CATGTGTGGCAGCTGGCTGCTCAACTCTGACCTTAGGTGATGCTCAGCTCTCATCTCCCAAGTGTGGGATGT
 ACAGCGGCTGAGCCACCGTGGCCAGCCCACTAATTTTGTATTTTATAGTAGAGACAGGGTGTACCAATGT
 TGGCCAGGCTGCTTGAACCTCTGACTCAGGTAACTGACCTGCTCCGCTCCCAAGTGTGGGATTTACAGG
 TGTGAGCCACACCGCCGCTACATATTTTTAAATTGAATCTACTATTTATGTGATCTTTGGAGCTCAGACG

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FIGURE 180

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPGRLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV
FPEKINGSVLPFGSGAPARLLCRLQAFGETLLLELEQDSGVQVEGLTVQYLGQAPPELLGGAE
GTYLTGTINGDPESVASLHWDGALLGVLQYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPCMNVKAPLGSPPRRRAKRFASLSRFVETLVVADDKMAAFHAGLKRILLTVMAA
AAKAFKHPSIRNPVSLVTRLVLGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLGMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRHVMAVMAHVDPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PVTFFPKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCLHMDQLQDFNI PQAGGWGPGWGPWGDSCRTCGGGVQFSSRDCTRPVPRNGGKY
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPFGMDWVPRYTGVAPQDQCK
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGDG
SGCSKQSGSFRKFRYGYNNVVTIPAGATHILVRQQGNPGHRSIYLAKLPDGSYALNGEYTL
MPSPTDVLVPGAVSLRYSGATASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
ESTPRPTQDQLHRRALILEILRRRPWAGRK

Important features of the protein:

Signal peptide:

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-
582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metalloproteinases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGTCTCTCAGTCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACCATGG
CAAAGAATCCTCCAGAGAATTGTGAAGACTGTCACATTCTAAATGCAGAAGCTTTTAAATCC
AAGAAAATATGTAAATCAGTTAAGATTTGTGGACTGGTGTGGTATCCTGGCCCTAACTCT
AATTGTCTCTGTTTTGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA
TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAAATTGATCCTGTG
ACCAGAACTGAAATATTCAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT
TAAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAACTCAGA
TTAAAGTGATTCTGAATTTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
ACAACCTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
TTTTCTTAAAAATTCCAAAATTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC
CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGAGAAGATCTTCACTTT
CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT
AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAAGGAAGAACTTCCAATAAATGACTATACTG
AAAATGGAATAGAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT
CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA
CTGCTACCAAGGAGGACGAGTCATCTGTCTGTGCATCATGCCTTGTAAGTGGTGGGTGGCCC
GCATGCTGGGGAGGGTCTTAATAGGAGGTTTGAGCTCAAATGCTTAACTGCTGGCAACATAT
AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT
CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC
AAAAAAAAAAAAAAAAAAAA

FIGURE 182

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT LIVLFWGSKHFWPEVPKKAY
DMEHTFYSGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTG IYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEI FDPMLDERGYCCIIYCRNRNRYCRRVCEPLLGYYPYPCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:

Signal peptide:

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCGGAAC TGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGGCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACCC**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCACTGCCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCGCGGCCCTCATGGTCATCTCCTGCCCTGCTCTCGGCATAGCCT
 GCGCCTGCGCCGTCATCGGGATGAAGTGCACGCGCTGCGCCAAGGGCACACCCGCCAAGACC
 ACCTTTGCCATCCTCGGCGGCACCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAAGTTCTACAACCCGCTGCTGCCCAGCGGCATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT
 GGCACCCTGCTTTGCTGTCTGCGCAGGACGAGGCACCCTACAGGCCCTACCAGGCCCCGCC
 CAGGGCCACCACGACCACTGCAAAACCCGCACCTGCCTACCAGCCACAGCTGCCTACAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTTCTCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTTACTTCTGGGCAATTTTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGAAATAAGAGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAAAATCCTGTCTGTTTTGTATTTATTATATATAT
 TTATGTGGGTGATTGATAACAAGTTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAAA

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FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITLILPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
 QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTTPAKTTTFAILGGTL
 FILAGLLCMVAVSWTTNDVVQNFYNPLLPSGMKFEIGQALYLGFISSSLIGGTLCLCLSCQ
 DEAPYRPFYQAPPRATTTTANTAPAYQPPAAYKDNRAPSVTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCCTCAGGAGCGCGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATCATGTCACACCACACATGCCAAGTGGTGGCGTTCCCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC
 CATGCTGCAGGCAGTGCAGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCTCC
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAGCC
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGCTGGAGT
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCGAGACTGTTTACAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGTG
 GCGTGGGTCTGGAGGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCTGCCCTGCCGGGG
 CCTGGCACCAAGAAGAAACCACTACAAGCCGTTTCTTATCATGCCCTCAGGCCACAGTGTG
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAAAACAGAAG
 ATATACGATGGAGGTGCCCCGACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA
 TGTGTAATGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCAAAAA
 AACAAGGAGATCCCATCTAGATTTCTTCTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTCC
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCTCAC
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCCTCCTAGTCAATAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAAACCTTTTGAAAGGAAAGAGTAGACCCAAAGATGTTATTTT
 TTGCTGTTTGAATTTTGCTCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTGAATCTCTCCAGCCATGATCTCGGTTTTCTTACACTG
 TGATCTTAAAGTTACCAAACCAAAGTCATTTTTCAGTTTGAGGCAACCAACCTTTCTACTG
 CTGTTGACATCTTCTTATTACAGCAACACCATTCTAGGAGTTTCTGAGCTCTCCACTGGAG
 TCCTCTTTCTGTGCGGGCTCAGAAATTGTCCCTAGATGAATGAGAAAATTATTTTTTTTAAT
 TTAAGTCCTAAATATAGTTAAATAAATAATGTTTGTAGTAAATGATACACTATCTCTGTGA
 AATAGCCTCACCCCTAGATGTGGATAGAAGGAAATGAAAAATAATTGCTTTGACATTGTCT
 ATATGGTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAAGCTCACACCTGTAATC
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCCAGAAGTTCGAGACTAGCCCTG
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTCGGGGAGGCTGAGGTGGGAGGATCACTTGAGCCCAGGG
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCCTGCACTCCAGCCAGGTGACATAGCGAGA
 TCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTTAGGAAGTAGGTTAA
 ACTAATCTTTAA

FIGURE 186

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734

><subunit 1 of 1, 261 aa, 1 stop

><MW: 27856, pI: 8.50, NX(S/T): 1

MSTTTQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACTCATC^{CC}CAGAGGATAAATGGCAACCCATGCCTTAGAAATCGCTG
 GGCTGTTTCTTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGGCCTTCATTGAAAAACAACATCGTGGTTTTTGAAAACTTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC
 TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCAAGGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGCGCAATGCCATCATCAGAGATTTCTATAACTCAATAGTGAAT
 GTTGCCCAAAACGTGAGCTTGGAGAAGCTCTCTACTTAGGATGGACCAGGCCTGGTGTCT
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTTGTTGCAACGAAAGAGCAGTAGTACCA
 GATACTCGATACCTTCCCATCGCACAAACCAAAAAAGTTTATCACACCGGAAAGAGTCAACG
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTGTATGTTTTTTAACTTTACTATATAAGC
 CATGCAAAATGACAAAAATCTATATTACTTTCTCAAAATGGACCCCAAAGAACTTTGATTTA
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACGTGTCATCAGCTATTTATGATTCTATAA
 GCTATTTACAGCAGAATGAGATATTAACCCAATGCCTTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTTTCTAAGGTGGTCAAGCATCTACTCTTTTATCATTTACTTCAAAATGACATTGCT
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG
 TCCATTACACTGAATAAATAGAACTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTTAAAAACAGCTTAGGGATTAATGTCTCCATTTATAATGA
 AGATTAAATGAAGGCTTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG
 TTTTTTAGCTTAGGAGTTAGAAATCCTAACTCTTTATCCTCTTCCAGAGGCTTTTTTT
 TTCTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCACAGGGCTTTGCATTC
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG
 GTTTTAGGAAAGTGAATAATTTTTGTTTTGTATTTGAAGAAGATGATGCATTTTGACAA
 GAAATCATATATGTATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC
 AATATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGCTTACCAAAAAACAACA
 ACAAAAAAGTTGTCTTTGAGAACTTCACCTGCCTATGTGGGTACCTGAGTCAAATTTG
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTGTGACCATTTCTGTTAGTTTTACTAAA
 ATCTGTAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAACTGACAATCCAATTTGA
 AAGTTTGTGTCGACGCTGTCTAGCTTAAATGAATGTGTTCTATTTGCTTTATACATTTATA
 TTATAAATTTGATATTTTCTAATT

FIGURE 189

TCGCC**AT**GGCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTGCGTGGTGCAGAGCACC GGCC
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGGCTTGTGGTCTACCTTGTGGGGC
CAAGTGTAACACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGTCACTCTGGGA
TTGTCTTTGTATCTCAGGGGTCTGACGCTAATCCCGTGTGCTGGACGGCGCATGCCATC
ATCCGGGACTTCTATAACCCCTGGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCTCCCT
CTACTTGGGCTGGGCGGCCTCAGGCCTTTTGTGTGGGTGGGGGGTTGTGTGTGCACTT
GCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCGCTACTCAACATCTGCCCC
GCCATCTCTCGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**GA**CGTGGAGGGGAATG
GGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTCTTTTACTGAGGATATTTAAATTCATTT
GAAACTGAGCCAAGGTGTTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTACCCCTTGG
ATGATGGAGCCAAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC
CAGTCAAGCTATGGAATAATGCGGAGGCTGCTTGCTGTGCTGGCTTTGCAACAAGACAGAC
TGTCCTCCAAAGAGTTCCTGCTGTGCTGGGGCTGGGCTTCCCTAGATGTCACTGGACAGCTG
CCCCCATCTACTCAGGTCTCTGGAGCTCCTCTTCAACCCTGAAAAACAAATCATCTG
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGTCTGATAAGACG
TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC
CTTCTGCCCTGCCCCCCCTCGTCTCACCCCTTTTACTCACATTTTATCAAATAAAGCATG
TTTTGTTAGTGCA

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FIGURE 190

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736

><subunit 1 of 1, 220 aa, 1 stop

><MW: 23292, pI: 8.43, NX(S/T): 0

MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLALPQDLQAARALCVIALLVALLFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLLIPVCWTAHAIRDFYNPLVAEAQKRELGASLYLGWAASGLLLGGGLLCCTCP
SGGSQGPSHYMARYSTSAPAISRGPSEYPTKNYV

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTTCTCTAGACTCAAAAGGCTTCCACGTTCTACATCTTG
AGCATCTTCTACCACTCCGAATTGAACCAAGTCTTCAAAGTAAAGGCAATGGCATTATTTATCCC
TTGCAAATTGCTGGGCTGGTTCTTGGGTTCTTGGCATGGTGGGGACTCTTGCCACAACCCT
TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC
TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTGCATGCAAGTCTA
TAGCTCCTTGTGGCTCTCCCGCTGCCCTGGAAACAGCCCGGGCCCTCATGTGTGTGGCTG
TTGTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCCTTCATCCTGAC
GGGTATCTTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA
ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA
AGCGCTGCTGTCTTCTTATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA
GAAGCAAGGTACAGATATCCAGTGCCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGCTTAAATGCCTCCTTTTGGCTCCAAGT
ATGGACTATGGTCAATGTTTTTTATAAAGTCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
GAACCTGCTTTATGTCTAGATTTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG
AATGAAAATGACTTACTTGGACATTCTGACTTCAGGTGTATTAATGCATTGACTATTGTTG
GACCAATCGCTGCTCCAATTTTCATATTCTAAATTCAGTATACCCATAATCATTAGCAAG
TGTACAATGATGGACTACTTATTACTTTTGGACCATGTATTATCTGATAAGAATCTAAA
GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

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FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRDfYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCCNRRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYV
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

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FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGCATGAAGATCACTGGGGGT
 CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
 AAAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA
 CATACTACCAAGTTTGTGGTTCTGACTACATCACCTATGGGAATGAATGTCACCTTGTGTACC
 GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGCTAAATTCTCCA
 TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCAGGCTCTGACTG
 AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTTCAGAGTAATCTTG
 ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
 TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCCAGA

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FIGURE 194

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739

><subunit 1 of 1, 85 aa, 1 stop

><MW: 9232, pI: 7.94, NX(S/T): 0

MKITGGLLLCTVVYFCSSEEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC

Signal peptide:

amino acids 1-19

FIGURE 195

CGCCGCC**ATGG**GCTGCCTCCCCCGCGCGGCTGCTGTCTTGGCCCTGACCGGGCTGGCGCTGC
 TCCTGCTCCTGTGCTGGGGCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA
 AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA
 ATTCCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCGGAGGTGC
 AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC
 ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
 CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG
 TCAACTACGATGACTACT**TAA**CCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATT
 TCTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTGCTCTATTTTCAGCAGAT
 CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAAAACAACATGTAAATGCCTTT
 TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTTAAAAAGA

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FIGURE 196

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742

><subunit 1 of 1, 148 aa, 1 stop

><MW: 17183, pI: 8.77, NX(S/T): 0

MAASPARPAVLALTGLALLLLLCWGGISGNKLKMLQKREAPVFTKTKVAVDENKAKEFL

GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNDRDRNGHEYYGDYYQRHYD

EDSAIGPRSPYGFRRHGASVNYDDY

Signal peptide:

amino acids 1-30

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FIGURE 197

CGGCTCGAGCCCGCCGGAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGGAGCCGGGCGCTC
GGTAGCGCGCGGGCAAGGCAGGCGCC**ATG**ACCCTGATTGAAGGGGTGGGTGATGAGGTGAC
CGTCTCTTTCTCGGTGCTTGCCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA
CCGCTGAGGGCGGGACCCACTGCCCCAGCCGTACGGGACCCCAACGCCATCCCAGCCAGC
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCCCAGGGGCAGAGACCCCCAGCCT
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGCACGGGGTTACAGCAACACCGCCAG
CCCCGGACTCCCCGAGGAGCCCTCGTGCTACGGCTGAAATTCTCAATGATTAGAGCAG
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGGACCCAGTTTCCCGGCCG
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG
GCAGCCTTACCTCCCTCCCACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC
CCAAATCCCCCTGCCCGCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT
GCTGCTGCCCTGCTGCTCCTGTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACACCTGCTCCTCAGTCTCCTG
GCCTTTGCCATGTACCGCCCG**TAG**TGCCTCCGCGGGCGCTTGGCAGCGTCGCCGGCCCTCC
GGACCTTGCTCCCGCGCGCGGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG
CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG
CCCCGCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA
CTGGGAGTGGGCTCCTCGGGGTGGGGCATCTGCTGTCGCTGCCTCGGCCCCGGGCAGAGCCG
GGCCGCCCCGGGGGCCCGTCTTAGTGTTCTGCCGAGGACCCAGCCGCCCTCCAATCCCTGAC
AGCTCCTTGGGCTGAGTTGGGGACGCCAGGTGGTGGGAGGCTGGTGAAGGGGAGCGGGGAG
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACTGTGAAGTTTAAAAAAAAA
AAAAAAA

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FIGURE 198

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQLGDDTQTLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

GAGATTGGAAACAGCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCTTAAGAACCATCAGCCC
TCAGCTGCACCTCCTCCCTCCAAGGATGACAAAGGCCTACTATCTATTTGGTFCAGAGC
TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
GAGGAGCTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCCTGGCTTTTGTGG
AAAGCAAGTTCAACATCTCAAAGATAAAATGAGTACGGGATGGAAGCTTTGACTATGGCCT
TTCCAGATCAACAGCCACTACTGGTGAACGATTATAGAAGTACTCGGAAACACCTTTGCCA
CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGCAAAAAGGA
TTGTGTCGGGAGCACGGGGGATGAACAACTGGGTAGAATGGAGGTGCACTGTTCAAGCCGG
CCACTCTCTACTGGCTGACAGGATGCCGCTGAGATGGAACAGGGTGGGGTGACCCGTGG
AGTCATTCCAAGACTCCTGTCTCACTCAGGGATCTTCAATTCTTCTTCTTCTACTGCCTFCA
CTTTCATCTGTTATTTTCTTCCCTTCCCATTACAACATAAAACTGACCAGAGCCCCAGGAATAAA
TGGTTTTCTTGGCTTCTCTTACTCCCATCTGGACCCAGTCCCTGGTTCTCTGTCTGTTAT
TTGTAACCTGAGGACCACAATAAGAAATCTTTATATTTATCG

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FIGURE 200

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLCVDCQDLLNPNLLAGIHCAKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

FIGURE 201

TCTGACCTGACTGGAAGCGTCCAAAGAGGGACGGCTGTGACGCCCTGCTTGACTGAGAACC
 CCAGCTCATCCCCAGACACCTCATAGCAACCTATTTATACAAAGGGGGAAAGAAACACCTGAG
 CAGAATGGAATCATATTTTTTTTCCCAAGGAGAAACCGGGGTAAGGGAGGGGAAGCAATTC
 AATTTGAAGTCCCTGTGAATGGGCTTTTCCAGAGGCAATTAAGAAATCCACTCAGAGAGGAC
 TTGGGGTGAACATTTGGGTCCTGTGGTTTCTGATTGTAAGTGGAGACAGGTCCTTGACACACGC
 TGTGTGCAAAATGTCAGGACAGGTTAAGTGACTGGCAGAAAAAATCTCCAGGTGGAACCAAGCA
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
 CTGTTGCATTTGGCAAGTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG
 CAGACTCCAGTTCTCCTGCTGCTCCTGATGCTGGGATGCTGCTGATGCTGGTGGCGATGT
 TGCACCTCCCCACCACACCTGCACCAGACTGTACAGCCCCAAGCCAGCAAGCACAGCCCT
 GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA
 GGGTGAAGAGTACAGCCCTCTGGAGGGCCTGCCACCCTTTATCTCACTGCGGGAGGATCAGC
 TGCTGGTGGCCGTGGCCTTACCCAGGCCAGAAGGAACAGAGCCAGGGCAGGAGAGGTGGG
 AGCTACCGCCTCATCAAGCAGCAAGGAGGACAGGATAAGGAAGCCCCAAGAGAGGACTGGGG
 GGCTGATGAGGACGGGAGGTGCTGAAGAAGAGGAGTTGACCCCGTTGACGCTGGGACCCAG
 GTGGCTCCAGGAGGCACTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCGAGGTGCGG
 CACCCACTGTGCTGCAGCAGCACCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
 TTTCCATGATGAGGCCTGGTCCACTCTCCTGCGGACTGTACACAGCATCCTCGACACAGTGC
 CCAGGGCCTTCCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG
 TCTGCTCTCAGCGAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAAGAG
 GCTGGTGCCGCCATGCGCCCGGATGCTGGGGGCCACAGAGCCACCCGGGATGTGCTCGTCT
 TCATGGATGCCACTGCGAGTGCCACCAGGCTGGCTGGAGCCCTCCTCAGCAAGAATAGCT
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA
 TTACCCCTCAAAGGACCTGCAGCGTGGGCTGTGGACTGGAAGCTGGATTTCCATGGGAAC
 CTTTGCCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
 GTGCCCGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAACACTGGAGCGTATGACTC
 TCTTATGTCGCTGCGAGGTGGTGAAAACCTCGAACTGTCTTTCAAGGCCCTGGCTCTGTGGTG
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTTCCCAT
 TCCCCCTCGACCAGGAGGCCACCCTGAGGAACAGGGTTGCGATTGCTGAGACTTGGCTGGG
 GTCATTTCAAAGAAACCTTCTACAAGCATAGCCAGAGGCCTTCTCCTTGAGCAAGGCTGAGA
 AGCCAGACTGCATGGGAACGCTTGCAGCTGCAAGAGAGACTGGGTGTGCGACATTCACCTGG
 TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGA
 GCTCCACAAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAGGGGACATCTGGGCT
 GTCCCATGGTGTGGCTCCTTGCAGTGACAGCCGCGACGACAGTACCTGACGACACACAGC
 AGGAAGGAGATTCACTTTGGCAGCCACAGCACCTGTGCTTTGCTGTGAGGCAGGAGCAGGT
 GATTCTTCAGAAGCTGCACGAGGAAGGCCATCCACCAGCAGCTGGGACTTCCAGG
 AGAATGGGATGATTGTCCACATTTCTTCTGGGAAATGCATGGAAGCTGTGGTGCAAGAAAAAC
 AATAAGATTTGTACCTGCGTCCGTGTGATGGAAGAAAGCCGCCAGCATGGCGATTGACCA
 GATAAATGCTGTGGATGAACGATGTAATGTCAATGTGAGAAAGAAAGAGAATTTTGGCCATC
 AAAATCCAGCTCCAAGTGAACGTAAAGAGCTTATATATTTTCATGAAGCTGATCCTTTTGTGT
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAGAATATAGGAAGTTTCTCCTTT
 TCACACCTTATTTTCATTGACTGCTGGCTGCTTA

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FIGURE 202

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
><subunit 1 of 1, 639 aa, 1 stop
><MW: 73063, pI: 6.84, NX(S/T): 2
MLLRKRYRHRPCRLQFLLLLLMLGCVLMMVAMLHPPHHTLHQTVTQAASKHSPPEARLRDLFG
ESQDWVLEAEDEGEESPLEGLPPFISLREDQLLVAVALPQARRNQSQGRGGSYRLIKQPR
RQDKEAPKRDWGADEDEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFKEIILVDDLSQQGQLKSALSEYVAR
LEGVKLLRSNKRGLAIRARMLGATRATGDLVLFMDAHCECHPGWLEPLLSRIAGDRSRVSP
VIDVIDWKTQYYPSKDLQRGVLDWKLDHFWEPLPEHVRKALQSPISPIRSFVVPGEVVAMD
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSEILPCSRVGHIYQNQDSHSPLDQEATL
RNRVRIAETWLGSKFETFYKHSPEAFSLSKAEKPDCEMERLQLQRRRLGCRTFHWFLANVPEL
YPSEPRPSFSGKLHNTGLGLCADCQAEGLDILGCPMVLAPCSDSRQQQYLQHTSRKEIHFGSP
QHLCFVVRQEQVILQNCTEEGLAIHQHWFQENGMIVHILSGKCMEAVVQENNKDLYLRPC
DGKARQQWRFDQINAVDER
```

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAAATCTGGGTACACAGCTGAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTGCCACCTCCTCCCTCTCTGGCCACTGCTGTTTGC
 TGCCCTCCACCGCTGCTCAGGGCTTTTCATCCTCCCTCGAACCCACAGCCCCAGCC
 CGCCCCCTGTGTGCCAGGGGAGGCCCTCGGCCCCACGTCATGTGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCCAGATCACGTCGGCAAGTCTGCTGGCCACTG
 CACCCACGACCCACCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGAGAGGGGACCCCACTCTGCCAATCCCGG
 ATTTCTGGACTATGTTTTGCGAGCCCTCATGGGCTCGCAACCCACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCCCTGGCGGCATT
 CTGTTCGGGGGCGCTGGGGAAGGTGTGGACCCCCAGCTCTATGTACAATTACCATCTCCAT
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCGCAGCCAGAAGC
 GACGCAGACCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGCACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTCGGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCGGCTGGGATGCCACCCCAAGGGGGCTCCAG
 CCTTCCAGTTGAACCGGTGAGGGCAGGGGCAATGGGATGGGAGGCAAGAGGGAAGGCAAC
 TTAGCTTTTCAGAGCTGGGGTGGGGGTGCCCTCTGGATGGGTATGAGGAGGCAGGCGTGGC
 CTCCACAGCCCCCTGGCCCTCCAAGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCCTC
 CTCTCCCAGTCTCTCAGGATCTGTGTCCTATTCTCTGCTGCCATAACTCCAACCTCTGCC
 TCTTTGGTTTTTTCTCATGCCACCTTGTCTAAGACAACCTGCCCTCTTAACCTTGATTCCC
 CCTCTTTGTCTTGAACCTTCCCCCTTCTATTCTGGCCTACCCCTTGGTTCTCTGACTGTGCCCT
 TCCCTCTTCTCTCAGGATTCCTCTGGTGAATCTGTGATGCCCAATGTGTGGGTGCAAGC
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCATCCCACTGAGGGTGGGGCAGCTGTGGGGA
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGCACACCACCCGGAACACTCCCCAGCC
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAGCCTTGCACACTCACCTCCACCTTCAC
 AGGCATTTCACACGCTCCTGCACCCCTCTCCCGTCCATACCGTCCGCTCAGCTGACTCT
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTTTCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCTGATGTTGTGGTGG
 TGTGCGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGAGCCCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCCTTGGGCTCCTATCGGTGATGG
 TCTCGTCCCATTCCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCAAGGATGCCGGCA
 TCACCTTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTCACCCCAAGCCCA
 CTGTGTAATACTGTTTTCTGACAGATGGGTTTTGGGGAGTCGCTGCTGCACTACATGAGAA
 AGGACTCCCAATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTGTCTGCTCTGGTGG
 TCTGTGTGTGTGCCATTCTCTGGACTTCAGAGCCCCCTGAGCGAGTCTCCTCTCCAGCCT
 CCTTTGGGCTCCCTAACTCCACCTAGGCTGCCAGGACCGAGTCACTGGTTCAGGCC
 ATCGGGAGCTCTGCCTCCAAGTCTACCCCTTCCCTTCCCGGACTCCCTCTGTCCCCCTCTT
 CCTCCCTCCTTCTCCTCACTCTCCTTCCCTTTGCTTCCCTGCCCTTCCCCCTCCTCAGGTT
 CTTCCCTCCTTCTCAGTGTTTTTCACCTTCCCTCCTTCCCTTCCCTTCCCTGGCTCCTAGGCT
 GTGATATATATTTTTGTATTATCTCTTCTTCTTCTGTGGTGATCATCTGAATTACTGTG
 GGATGTAAGTTTCAAAATTTTCAATAAAGCCTTTGCAAGATAA

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FIGURE 204

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASFPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACQQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

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FIGURE 205

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCCGCTGCCCTCACTCCCGGCCAGG**ATGG**
 CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG
 CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC
 GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGGAGCCCGTGGACACCGGTCCCC
 CAGCCCCCACCCTCGCGCCAGGACCCGAGGACAGCACCAGCGCAGGAGCGGCTGGACCAGGGC
 GCGGGGTCGCTGGGGCCCGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG
 CGTGGTGCTGGCGCTCGTGGTCTGCGCGCTGAGAAAGTTTTCTGCCTCC**TGA**AGCGAATAAA
 GGGGCCGCGCCCGCGCGCGCGCGACTCGGCAAAAAAAAAAAAAA

FIGURE 206

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCCGTTGGTTGGTGCGCGGCTGAAGGGTGTGGCGCGAGCAGCGTCTGTTGGTTGGCCGGCGG
CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCCA
CGGCTGTCTGCACTGCCACAGCAACTTCTCAAGAAGTTCTCCTTCTACCGCCACCATTGTGA
ACTTCAAGTCTGTTGGTGGGCGACATCCCGTGTGAGGGGCGCTGCTCACCAGCTGGAGC
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCGGGAGAAGCTGGA
CCAAGTGGCGACAGAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC
CCGGGTATTTCCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCCTAAGTAGCCC
CCAGAGGGCGTGGGAGTGTGCCACCGCCCTCCCCTGAAGTTTGCTCCATCTCACGCTGGGG
GTCAACCTGGGGACCCCTTCCCTCCGGCCATGGACACACATACATAAAAAACAGGCGCAT
CGACTGTGACACCGCTGTGGCATCTTCCAGTACGAGACCATTCTCTGCAACAACATGCACAG
ACTCGACGTGCGCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCGATCACACCCACCCGT
GCCAGGGCCCTACTGTCCCTGGGGTCCCAGGCTCTCCTTGAGGGGGGCTCCCCGCTTCCAC
CTGGCTGTCACTGGGTAGGGCGGGGCGTGGGTTAGGGGCGCACCACTTCCAAGCCTGTGT
CCCACAGGTCTCGGCGCAGTGGAAGTCACTGTCCAGGGCTCTGAACTACATAAATAAC
TGGCACAAGTAAGTCCCCCTCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG
GGTGAGTATGTGTGGGGCAGAGCTGGCTCCCTCAGCTCCCACGTCTTAGAGGGGCTCCCGA
GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGCGGCTGCAGTCTTTTCTCCCTCAAAG
GTCTCCGACCCCTCAGCTGGAGGCGGGCATCTTTCCTAAAGGGTCCCCATAGGGTCTGGTTCC
ACCCCATCCAGGCTGTGGTTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC
ATGGAGGGGCTACTGCCCCACATTGCCTTTTCAGACAGGACACGAGCATGAGGTAAAGCCGC
CTGACTGTGAGCTACAGGGGGAGGGGTAAAGGGAGAGAGGAGGGGGGTAGGGGGTCTCT
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGTGGATGTAC
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCACGCTCCTCTGCCTTCTCTGG
CCTGGGACACACAGAGCCACCCCGCCTTGTGAGTGACCCAGAGAAGGGAGGCCTCGGGAGA
AGGGGTGCTCGTAAGCCAACACAGCGTGC CGCGGCCTGCACACCTTCGGACATCCAGGC
ACGAGGGTGTCTGGATGTGGCCACACATAGGACCACACGTCCCAGCTGGGAGGAGAGGCCT
GGGGCCCCCAGGGAGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC
CCGACGCTGGTATCGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCGAGGGCAAC
GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC
CTCAGGACCCCTCTCCGACCCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG
GAGGGAATGGGGTGGGCTGTGCGCAGCATCAGCGCTGGCAGGTCCGACAGCTGCGGA
TGTGATTAAGTCCCTGATGTTTCTC

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FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDL P
```

Signal peptide:

amino acids 1-15

FIGURE 209

AGCAGGAGCAGGAGAGGGGACAATGGGAAGCTGCCCGTCCAGGTTTCATGTTCTCTTATTTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTCGCTGGTAGACAATGAACAACTG
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAATTGAGCCGTTTCATTGAGAT
 CAACAGCCTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAGATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAATG
 CACAGATACCAGAAGGCAGCCAAGCTCTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTTTCAAATAAAGGAGTCTCAACTGCCAG
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC
 GTAGAGCATGTGCAAAACTTTTGTGATGGATTCCCTAAGTGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAACCTCTGAATTTCTCCTTGGAATAACATATGGCC
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACGACGTCACACACGACGACGACGCGTGACAC
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAATCTCGTTTTCTC
 TTCTTCCTTCTTTTAAATTTATATCCTCACTCCCTATCCAATTTCTTCTTATCGTGCATT
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTTCCTGCTCTTTAAGGTTACCTAAGGGT
 TGAACCTCTACCTCTTTTATAAGCACATGTCCGCTCTGACTCAGGATCAAAAACCAAGG
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTGGCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACCTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCC
 TATGTAAATCAACAACCTGCATAATAAATAAAGGCAATCATGTTATA

FIGURE 210

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSFSGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA
KLFQGGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDWDTLPTAEVSVHEVQNF
CDGFLSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGGCGCGGGTG
GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCGGGGACCCGGGCTCAGG
GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACCAATGGCAGCGTCCGCCGGAGCCGGG
GCGGTGATTGCAGCCCCAGACAGCGGCGCTGGCTGTGGTCGGTGCTGGCGGCGGCGCTTGG
GCTCTTGACAGCTGGAGTATCAGCCTTGGAAGTATATACGCCAAAAGAAATCTTCGTGGCAA
ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCGACACTACTGTGTGCTTTTTTCCACTACTC
CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG
ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAAATATGCAGTTTATACACAATGGCACC
TATATCTGTGATGTCAAAAACCCCTCCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
TGTGCTAGAAAAAGAGAATTTGCCTGTGTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG
CTGTGGTCCTAGGCTCTACTCTGCTCATCAGCATCAGAGAGTTTGTACCAGTTAAGCAGGC
AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC
TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAAGAGTCTGCCTTCTGGATCTCACC
AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAATTAAAGAGAATACCTAGAACATATC
CTCAGCAAGAAACAAAACCAAACTGGACTCTCGTGCAGAAAAATGTAGCCCATTTACCACATGT
AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT
ACAAAGGATATGTATAAATATTTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTTCATGA
TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTTGTCTTTTTTGTACTTTCTTTTC
AGGTCATTTACAATTGGGAGATTTAGAAAACATTCCTTTTACCATCATTTAGAAAATGGTTTG
CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAACTAAG
GGCTTAAGACTGATTAGTCTTATGACATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
GCATACCCAGGGTGGCCTTTAGCACAGTATCAGTACCATTATTTGTCTGCCGCTTTTAAAAA
AATACCCATTGGCTATGCCACTTGAAAACAAATTTGAGAAGTTTTTTTTGAAGTTTTTCTCACT
AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCCTTG
AAATGTGTCATATCAATTTCTGGATTATAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
GTCACTTCAATTCGGACACAGTTGGATCAATACTGATTAAGTAGAAAAATCCAAGCTTTGCTT
GAGAAGTTTTGTAACGTGGAGAGTAAAAAGTATCGGTTTTTA

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FIGURE 212

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510

><subunit 1 of 1, 269 aa, 1 stop

><MW: 29082, pI: 9.02, NX(S/T): 3

MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGTTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKASININ
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDTGCTSESLSVPKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSKINKSESVVYADIRKN

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTGACAGTGAAGTCCCGGGCTGCCGCC
 CCCGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGTCCATCAGCGCGCCGGGTGCCGCC
 TCTCGGCCACGGCTGGGTGCGGGGCTCGGGTGGGGCTGGGGCTGGCGTCCGGGTGAAGC
 TGGCAGGTGGGCTGAGGGGCGCGGCCCGGCGCAGTCCCCCGGGCCCCGACCTGAGGCG
 TCGCCTCTGGCCGAGCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGCAGACCCGGC
 GCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGAAAAGAAGTC
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGTGACCATGTAAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGAATTCTG
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAGCCTTGAAGATGA
 TGAAAGAGAATGTTGCATTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT
 ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGGAATTCAAACCTGGCAAGAA
 AAAGAATGATTTTGAACAAGGCGAATTATATTGAGAGAAAAGTTGAAAATTCATTGAAT
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA
 ACTTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTGGA
 CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTTACAATAGAGCAAGGTAATGAATACTTCTGCTGTGCTAGCTATATCGCATC
 TTAACACTATTTTATTAATTAAGTCAAAATTTCTTTGTTTCCATTCCAAAATCAACCTGC
 CACATTTTGGGAGCTTTTCTACATGTCTGTTTCTCATCTGTAAGTGAAGGAAGTAAACA
 GTTTTATAAAGTAAAAAA

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FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPSCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

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FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG
 AGGCTGGTGGGAAGAAGCCGAGATGGCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCGGGCAGCGGCTGCCGGGCCGGGACT
 GGTGCGCGAGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTACAGCGGCAGCTCAGCAGGAGGAGCGGGGC
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG
 TGGAGTCGCACCTGTGCGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC
 GTGTCGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCAGGAGCAGAAG
 TCCTTCTTCGCCAAATACTGGATGTACATCATTTCCCGTCGTCTGTTCTCATGATGTCAGG
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCTCCCTGTAAGTCTATTTAAAAACATCGACGATACATTGAAATGTG
 TGAACGTTTTGAAAAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCAGTGCTCACTTGATACGTTATTCAGAAACCCAAG
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT
 TAAACTGTCCCCCAGATCGACACGCAAAAAAAA

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FIGURE 216

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRRPGALDGLEA
GGYVSSFVPACSLVESHLSQDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGSGLCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCAGCGGGGAGGGTGGCCTGGCGGCCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCGCAGACCGGGGCAGCAGGTGCTCCGGGGGCCACC
ATGCTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTTCCTTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTTCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAACTCTACCAGCATTACTACTTCTGGAAGGTCAAATTGCCATCCTCTATGTCTG
 TGGCCTTGCTCTACAGTCCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC
 GCAAGAATTCTTGTGCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACTCTCT
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTTCGAGGCCTGGTATATCCATGAGCAGCTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTTGCTCGAGCTGCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTTGTGGCTGC
 CATCCCTCTCCTGGCTCTGGCAGGGGCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC
 GGCAGCGTGCCTTCTCAAGGACCTGTGCTGGAGGCCTGCCTGCCTCCTGTGGACCGCCGC
 GTGCTGCTGCTGGGCACCATACAAGCTCTATTTGAGAGTGTCACTTTCATCTTTGTCTTCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTTGTGTGCTCATCGTCGTCTTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTTCATAGCCTTTTCTACTTATTGAGT
 TGGCTTGTGGATTATACCTTTCCAGCATGAGCTTCCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTGTACTCAACTGGTTCGGGTACCTCTGCACTCACTGGCTTGCCTAGGGCT
 CCTTGTCTCCTGCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACAGATTGCTCTG
 CTGTGATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTCACCGTGGTAAGGCATGATGCT
 GAGTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTGTAACCCCACTCCAG
 GACAAGATAGCTGGGACAGACTCTTGAATTCCAGCTATCCGGGATTGTACAGATCTCTGTG
 GACTGACTTTGTGACTGTCTGTGGTTTCTCCTGCCATTGCTTTGTGTTTGGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGTGCACAAAAGTTCCCTCTGTGTTACTCCCATTTAGAAA
 ATAAACACTTTTAAATGATCAAAAAAAAAA

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FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY
LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPMSFLRRKVIPET
EQAGVLNWFRVPLHSLACLGLLVLHSDRKTGTRNMFISCSAVMMALLAVVGLFTVVRHDA
ELRVPSPTTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

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FIGURE 219

GCGACGCGCGGGCGGGCGGCGAGAGGAAACGCGCGCCGGGCGGGCCCCGGCCCTGGAGATG
GTCCCCGGGCGCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCCTCGCGGCCCA
CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCTGGGGACATTCGATACA
TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT
CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCA
GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC
AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC
GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTCTGCTCGG
CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT
CCATCCCAGTCAATGTCAACAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC
TGGTAGAAGAGTGTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
AGGAATTTTGCTACTTTGGAATTTGGAGATAGCATCTGGGGACAAGTGGAGCCAGGTAGAGGA
AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCCAGG
GCCCCAAGGGTGCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA
GAACCCGAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACT
CACCTGGCTCCAGCCTCCCTATCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG
AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA
GCTTCTCATCAGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 220

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532

><subunit 1 of 1, 188 aa, 1 stop

><MW: 21042, pI: 5.36, NX(S/T): 2

MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:

amino acids 1-20

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FIGURE 222

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGLYKDNKSSIHCMDSLQRYCLMAVFNVIYLENEDSE

Important features of the protein:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

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FIGURE 223

CTCGCTTCTCCTTCTGGATGGGGGCCAGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG
GGTGCCCGGCACAACACAGACGCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT
GGCCCTGGAGGAGGCAAGTATTTGAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGCTGTAGGTCTTCTCCTGGTAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTTGTCGCCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACCTACCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAAGTGGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAA

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FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGGNTQEVTLQPGYITKVFVAFQAFLRGMVMTSKDRIFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYANSPPVGR
```

Signal peptide:

amino acids 1-22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGGAAGCTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAATACATCATGTTTTTCGATAAGAAGAAATTTAGGATCCAGTT
 TTTTTTTAAACCGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTGGGATT
 TATTTGTCTTGGAGTGTTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAACTCGGTCCATCT
 CCCAAGGGGTCCAATTTTTCTCTCTGGGTGTGAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGGCTGTCAATGCAACTGGCCCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTTGAA
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTTACTGACAATGCTTCTCTCTGCGGAACGAGGATGCCCTAAGGGGTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGCTATAACAGCCTTCAAAAACCTAAGTATAAT
 CAATTTAAAGGGCTCAACCAGCTCACTGGCTATACCTTGACCATAACCATATCAGCAATAT
 TGACGAAAATGCTTTTAAATGGAATACGACAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA
 TCTCCTATTGTTCTTAAACAATACCTTCAGACCTGTGACAAATTTACGGAATCTGGATCTGTCC
 TATAATCAGTGCATTCTCTGGATCTGAACAGTTTCGGGGCTTCGGGAAGCTGCTGAGTTT
 ACATTTACGGTCTAACTCCCTGAGAACCATCCCTGTGCGAATATTTCCAAGACTGCCGAACC
 TGGAACCTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAAATCAATTTTCCAAGCTCAACCTGGCCCT
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCACTGGAATAAAATCAGTGTCTAG
 GACAGACCATGTCTGGACCTGGAGCTCCTTACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTTTCAGTGGACCCAGTGTTTTCCAGTGTGTCCCGAATCTGCAGCGCTCAACCTGGA
 TTCCAACAAGCTCACATTTATTTGGTCAAGAGATTTTGGATTCTTGATATCCCTCAATGACA
 TCAGTCTTGCTGGGAATATATGGGAATGCAGCAGAAATATTTGGCTCCCTTTAACTGGCTG
 AAAAGTTTTAAAGGTCTAAGGGAGAATACAATTATCTGTGCCAGTGCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAAGCCCAAGCTCCCCAGGCCGAAGCAT
 GAGAGCAAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTTCTGTCCG
 TGCTCGTCATCTGTGGTTATCTACGTGTCTGGAAGCGGTACCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT
 GACTCCAGCACCCAGGAATTTTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAAGTGGTGCTTTATTGAACTC
 TGGTGACTATCAAGGGAACCGGATGCCCCCTCCCTTCCCTCTCCCTCTCACTTTGGTGG
 CAAGATCCTTCTCTGTCCGTTTTAGTGCATTCAATAATCTGGTCAATTTCTCTCATACATA
 ATCAACCCATTGAATTTAAATACCAACAAATCAATGTGAAGCTTGAACCTCCGTTTAAATATA
 TACCTATTGTATAAGACCCCTTTACTGATTCCATTATGTGCGATTGTTTTAAGATAAAACT
 TCTTTCATAGGTAACCAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop .
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGKMVYCESQKLQEI PSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKEHLHLEHNQFSKLNALFPRLVSLQNLYLQWNKISVIGQTM
SWTWSSLQRLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNSNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTIICASPKELGQVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIITAGSVALFLSVLVI
LLVIYVSWKRPASMKQLQQRSLMRRHRKKRQSLQKQMPSTQEIFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCCTT
 TAAAT**ATG**TCAGATCCAGACTTTTCAGTGTACCTCAGCGATCTCAACGATAGGGATCTTG
 TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG
 TGGCAGCTCTTCTCTGTGGAGCTGTGGTCTCTGCCCTCCAGTGCTGGCTGAGGAGACCCGA
 ATTGATTCTCACAGGCGCACCATGGCAGTTTTTGTGCTTGGAGACTTGGACTCTATTTATGG
 GACAGAAGCAGCTGTGAGTCCAACCTGTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGCTCCATGTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCT**TGA**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA
 AAACATCAAATTTAGGAATAGTTATTTTCAGTTGTTGGAAATGTCCAGAGATCTATTATATA
 GTCTGAGGAAGGACAATTCGACAAAAGAATGGATGTTGGAAAAAATTTTGGTCATGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC
 AACCAAAATTAATGCTTCTCCACTAGTATCCAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC
 CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT
 CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC
 CTTTTCAGTAATGAATGTGGCCTCCATAGTCCATAGTGTCTCTGAGCCTCAGGGCTTG
 GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA
 CAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAAATTTGTTGAACAAAACAAT
 AAACATCAATAGATATCTAAAAA

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FIGURE 228

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303

><subunit 1 of 1, 146 aa, 1 stop

><MW: 16116, pI: 4.99, NX(S/T): 0

MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDEMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIHLQTQTPDLYP
VPAPCFGLGSPPPYEEIVKTT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGCGGAGTAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCACCCACC GGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGACGCGAGCTGACGCCCGCTTATTA
 GCTCTCGCTGCGTCGCCCCGGCTCAGAAGCTCCGTGGCGCGCGGCGACCGTGACGAGAAGCCCC
 ACGGCCAGCTCAGTTCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT
 CCCTCTTCAAACTCATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTTGCTGAAG
 ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGTCTTGATTGTGGC
 TTACCTCAAGTTACCATTTTTTCAGTCAAGTCTGTTTGTGTTGCTTCTTCAGAAATGTTTTTA
 CAATCTCAAGAAAAATATGTCCCAGAAATTGAGTTTACTGTTGCTTGATTGGAAGTCAATT
 TGGGATTGATGTTTACTGCACATATACTTTTCAACAACCAAGACATCAAAGCAGGTCAAGTT
 ACGTGAGCAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAATAAGA
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGCGAGGATATGCGGATCTGAAAAGAACAAAT
 GCTGTCCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTTGTGAATGGCTCAGCAGCCAAACACCACCAATGTTACTAGTGGGAATTTGGTGCCAGTAA
 CCACAATAAAAAGAACGAATGTCTCGGGCAGTATCAGATAGCAGTTGAAAATCAGCTTTGTGC
 TGCTCCATCCACTGTGGATTATATCCTATGCGAGAAAAGCTTTATAATTGCTGGCTTAGGAC
 AGACAAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAAAC
 TCTAATTCGTACATAAAAAATTTTAAAGTTATTTGTTTGCTTTACGGCAAGCTCTGTTCAATG
 CTGTACTATGTCTTAAAGAGAAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT
 TTTGTATAAATCTTTTGTGTTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATTTC
 ATTTCTATAACACATTTTATTTAAGTATATAACACGTTTTTTGGACAAGTGAAGAAATGTTTAA
 TCATTCTGTCATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAAATGTG
 CTTATTGTACTATATTTTGTATTCCAAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA
 TAATGTTTTGAAATCATGACCCAAAGAATGTATTGATTTGCACATATCCTTCAGAAATACTGA
 AGGTAATTATTGTATATTTTTTAAAAATTACACTTATAAGAGTAACTCTGAAATGATGATG
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAAATAGTT
 GTAACTCTAATCTTATACTTATTGAAGAATAAAGATATTTTTATGATGAGAGTAAACAATA
 AAGTATTCATGATTTTTCACATACATGAATGTTTCATTTAAAAGTTAAATCCTTTGAGTGTCT
 ATGTATCAGGAAAGCACATTTATTTCCATATTTGGGTTAATTTTCTTTTATTATATTGGTC
 TAGGAGGAAGGGACTTTGGAGAATGGAACCTTGAGGACTTAGCCAGGTGTATATAATAAAA
 GGTACTTTTGTGCTGTCATTAAATTGCTTGGAAAGTGTTAACATTATATATATAAGAGTATC
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCAATTTATATAATGGCCAC
 TTAAAAATAAGAACATTTAAAAATATAAATATGAAGATTGACTATCTTTTCAGGAAAAAGCT
 GTATATAGCAGAGGAAACCTTAATCTTTGGGTAAATCTAGATATAAAACAATATACTTTTAT
 TTAATTTCCCTTTAGCAAACTAATTGCCACATGGTGCCCTATTTTCATAGTATTTATT
 CTCATAGTAAC TGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT
 TGTATTGTTGCTCATTATAATATGCTACCACATGTAGCAATAATTAACAATTTTTATTAAAA
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAATCTCTCTTCTCTCTCTGTA
 CTGCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT

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FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLDDILQRLVKLENKVDYIVVNGSAANTNGTSGNL
VPVTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGCGGGGCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGC'TTCCAGCCCCAC
CATGCCGTGGCCCCGTGCTGCTGCTGCTGGCCGTGAGTGGGGGCCAGACAACCCGGCCATGCT
 TCCCCGGGTGCCAATGGCGAGGTGGAGACCTTCGGCCTTTTCGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGGCCA
 CTTGGACCTGTCTCCAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCGGGCT
 ACACGACGTTGGCTGGCCTGGATCTCAGCCACAACCTGCTCACCAGACTCTACCCACTGCC
 TTCTCCCGCCTTCGTACCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC
 AGCCGAGAGCTTCACCAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG
 AGGTCTCAGTGTCTGCCCTCAGCAGCACAGTCAGGGCCGGCTACACGTGACCTCTCC
 CACAACCTCATTACCCGCCTCGTGCCCCACCCACGAGGGGCGGGCTGCCGTGCGCCACCAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCCAACCTCCGAGACTTGCCCC
 TGCGCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTTCCGTGAGCTACCGGCCCTGCAGGTCTTGGACCTGTCCGGGCAACCCCAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTTAGGCCCTGAGCTCCCTGCGGAGCTGGACCTTTTCGGGCACC
 AACCTTGTGCCCCGTGCCGTGAGCGCTGCTCCTCCACCTCCCGGCTGCAGAGCGTCAGCGT
 GGGCCAGGATGTGCGGTGCCGGCGCCTGGTGCGGGAGGGCACCTACCCCGGAGGCGCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCCACC
 ATCTT**TGACA**CAATGGTGTGGCCAGGGCCACATAACAGACTGCTGTCTGGGTGCCTCAG
 GTCCCGAGTAACCTATGTCTCAATGTGCCAACACCAGTGGGGAGCCCGCAGGCCTATGTGGCA
 GCGTACCCACAGGAGTTGTGGGCTTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC
 AAAGTCTCACCCCTTTGTCTACGTTGGCTTCCCCAAACCATGAGCAGAGGACCTTCGATGCCA
 AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCCTTCCCTCAT
 GCCTGGGCCGGCCTGACCCGCAATGGGCAGAGGTTGGGTGGGACCCCTGTGCAGGGGCAGA
 GTTCAGGTCACCTGGGCTGAGTGTCCCTTGGGCCCATGGCCAGTCACCTCAGGGGCGAGTT
 TCTTTTCTAACATAGCCCTTTCTTGGCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAAGAATCAAGTCCACCCCTTCTCATGTGAC
 AGATGGGGAACCTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCCTGCGGGCAGTGCC
 ATGACTGGAGCACAGCCTCCTGCCTCCAGCCCGGACCCCAATGCACCTTTCTGTCTCCTCTA
 ATAAGCCCCACCTCCTCCGCTGGGCTCCCTTGTGCCCTTGCTGTTCCTCCATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGACCTCACAAAGTGGGACTCTGGGCCTCTGACCAGCT
 GTGCGGCATGGGCTAAGTCACTCTGCCCTTCGGAGCCTCTGGAAGCTTAGGGACATTGGTT
 CCAGCCTAGCCAGTTTCTCACCTGGGTGGGGTCCCCAGCATCCAGACTGGAAACCTCA
 CATTTTCCCTGAGCATCTCTAGATGCTGCCCAAGGAGTTGCTGCAGTTCTTGACCTTCA
 TCTGGCTGGGATCTCCAAGGGGCTCCTGGATTACGTCCCCACTGGCCCTGAGCACGACAGC
 CTTCTTACCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGAGCCATGCTATGCT
 TCTACCCCGAGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTCTCTTAGTCTTCACTTTTA
 TAAAGTTGTTGCCTTTTTAACGGAGTGTCACTTTCAACCGGCCTCCCTACCCCTGCTGGC
 CGGGGATGGAGACATGTCAATTTGTAAGCAGAAAAAGTTGCAATTTGTCACTTTTGTAAAT
 ATTGCTCTGGGCTGTGTTGGGGTGTGGGGGAAGCTGGGCATCAGTGGCCACATGGGCATC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAGCTCTGTCTTCCCCACCTGCGTAGC
 CCATCATCTATCAACCGGCTCTGATTTAATAAACACTATAAAAGGTTAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 232

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLTSISPTAFSRLRYLESDDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLEALLHLPALQSVSV
GQDVRCRRLLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTTCTGTGAGATTTCGATTTCTCCCAAGTTCCTTGTGGGTCTGAGG
 GGACCAGAAGGGTGAAGCTACGTTGGCTTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATTCCTCA
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAAGTCAAGCTGAAATCTTCTCTTAC
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGG
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACATTATACTCTCC
 GGAAGATCAGCAGCCTCGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGAA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCATCTCTTTACT
 GTACTAGTCTTGTGCTGGTCAAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGAT
 TGCTCTTATGCATCCCCAATCTTAATTGAGACCATACTTGTATAAGATTTTTTGTAATATCTT
 TCTGCTATTGGATATATTTATAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT
 ATTTTCTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG
 AGCAGGTGATGTATTTTATACAGTAAAAAAAAAAACCTTGTAATTTCTAGAAGAGTGGCT
 AGGGGGTTATTCATTTGTATTCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA
 TATTTGAAATTGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGTGTAT
 CTTCCAGCCAGGAATCTACACGGCCAGCATGTATTTCTACAAATAAAGTTTTCTTTGCATA
 CCAAAAAAAAAAAAAAAAAA

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FIGURE 234

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNGGATTCATNSHSDSELRP
EIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP
DHYTLRKISSLANSEFLTIIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAADVVKALG
ELDILLQWMEETE

Important features of the protein:**Signal peptide:**

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCGCTACTGCTGA**ATGT**CCGTCGCCGAGGAGGAGGAGAGGCTTTTGCCG
CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC
CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAAATGCAAGGAGAAGCAG
CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCGCACA
GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTTGGCAAGGAGTGACACCCGCCAT
TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG
TGTTTGGCAAAAGTGAAGATGAGCATTATCCCTTTGGAAATCAGTCATTGGAGGGATGATG
GCTGGTGTTATTGGCCAGTTTTTAGCCAATCCAACCTAGTAGTGAAGGTTGAGATGCAAAT
GGAAGGAAAAAGGAACTGGAAGGAAAACCATTGCGATTTTCGTGGTGACATCATGCATTTG
CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTTGGGCAGGCTGGGTACCCAATATACAA
AGAGCAGCACTGGTGAATATGGGAGATTTAACCCTTATGATACAGTGAAACACTACTTGGT
ATTGAATACACCCTTGAGGACAATATCATGACTCACGGTTATCAAGTTTATGTTCTGGAC
TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTCATCAAAAGCAGAATAATGAATCAACCA
CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTGAGGCTGT
TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTTACCATCTTGCTGAGAATGACCC
CTTGGTCAATGGTGTTCTGGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
TTTT**TAA**

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FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFGKSEDEH
YPLWKSIVIGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC
 GCCTGAAGTCGGCGTGGGCGTGTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC
 TTAAGAAGTAAAAATGGCAGGCTTCCTAGATAATTTTCGTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTCGCAGGTATATTGTTTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT
 TCACACATGTGGTGTATTTTCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATTCTTTTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACCTTA
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTGTAGATAGGTTTTTATCTCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAATGTTTTGTTTCTTACATTTTATGTTC
 TGAGTTTGAAATAGTTTTATGAAATTTCTTTATTTTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATCTGAGATTTAGAA
 CTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCACTTTTAGAAGTAACCACTCTTGT
 CTCTCTGGCTGGGCACGGTGGCTCATGCCTGTAATCCAGCACTTTGGGAGGCCGAGCGGG
 CCGATTGCTTGAGGTCAAGTGTGTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT
 AAAAAATACAAAATTAGCCAGGCATGGTGGTGGGTGCCTGTAATCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC
 TGCACCTAGCCTGGGGGAGAAAGTGAACCTCCCTCTCAAAAAAAGACCACTCTCAGTATC
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTGGTAAAGA
 AAAAAATATTGTTCTTATGTATTGAAGAAGGTACTTTTATATAATGATTTTTTAAATGCC
 AAAGGACTAGTTTGAAAGCTTCTTTTAAAAAGAATTCCTCAATATGACTTTTATGTGAGAA

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FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWMIDAADVYPKPEQLNHAFTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFG RTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCCCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTCAGAAGCTGGCCCAGGGTGGT
 GGTGAGCTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG
 GGAAGTGGGAGCCTCGAGCCCTCGGGTGAAGCTGACCCCAAGCCACCCCTCACCTGGACAG
GATGAGAGTGTGAGGTGTGCTTCGCCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA
 TGTTTATTCTGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACTACTTTGCGTTTAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT
 GCTTTGAAGACCGCATGATCATGAGTCTGTGAAAAACAATGTGGGCAGAGGCCATAACATC
 GCCCTGGTGAATGGAACCACGGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCACCTGGTGTGGTGG
 CCTCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAACTCTTCTCTGACTTG
 GGGAGTTCCTACGCAAAACAACCTGGGCTTCGGGACAGCTGGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGGTAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTTTTAGGGGTGGC
 TGTGGCTCTTCTCAGCCAGGGGCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCG
 GCAGGGGCTGAGGAGGAGAGCAGGGGGTGTGCGTGGAAGGTGCTGCAGGTCTTGCACGC
 TGTGTGCGCCTCTCTCTCGGAAACAGAACCCCTCCACAGCACATCTACCCGGAAGACC
 AGCCTCAGAGGGTCCTTCTGGAACAGCTGTCTGTGGAGAGAATGGGGTGCTTTCGTGAGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA
 TTTTGTGCTGTTTGAIAAAAAAAAAAAAAAAAAAAAA

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FIGURE 240

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24963, pI: 9.64, NX(S/T): 1

MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
 ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG
 DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFSDLGSSYAKQLGFRDSWVFIGAKD
 LRKSPFEQFLKNSPDTNKYEGWPPELLEMEGCMPPKPF

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop).

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCTCTGGGGAT
 CCAGAAACCCATGATACCTACTGAACACCGAATCCCTGGAAGCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTCTGCTGTCTAGTCTCTAGTCTCAAATTCAGTCCCTCC
 CTGCACCCCTTCTCTGGGACACTATGTTGTTCTCCGCCCTCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCTGAGTGTGGAAACAATGCCAGTCGCCCATCGATATTCAGACAGACAGTGT
 GACATTTGACCTGATTTGCTGTCTGCAGCCCCACGGATATGACCAGCCTGGCACCAGGC
 CTTTGGACCTGCACAACAATGGCCACACAGTGCAACTCTCTCTGCCCCCTTACCCTGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCATGGGGTCAGAAAGGATC
 CCCAGGGGGGTGAGAACACCAGATCAACAGTGAAGCCACATTGTCAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCCTCAGGGCTGGCT
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCTCCCTTCAACCTAAGAG
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGGTCCCAGATTTCATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTATCCAAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG
 CCTTCTCTGGCTGTTTATTTTCATTGCTAGAAAGATTGGAAGAAGAGGCTGGAAAACCGAA
 AGAGTGTGGTCTTACCTCAGCACAAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCA
 TGGATGTGGATGACTTCCTTTCATGCCTATCAGGAAGCCTCTAAAATGGGGTGTAGGATCTG
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCTTCCCTGGACATCTCTTAGAGAG
 GAATGGACCCAGGCTGTCAATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACCTCTGTTTAGTTGACGGG
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTCCCTAGATA
 TACTGCGGGATCTCTCCTTAGGATAAAGAGTGTGCTGTTGAAGTTGTATATTTTGTATCAATA
 TATTTGGAATTAAGTTTCTGACTTT

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FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWYEGPHGQDHWPFASYPECGNNAQSPIDIQTDSVTFDPDLF
ALQPHGYDQPGTEPLDLHNNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGPGGSEHQ
INSEATFAELHIVHYDSYDSLSEAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNRLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTI
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

[illegible]

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FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQSNQVFPSLSLIPLTQM
 LTLGPDHLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPIFVTQLGAQGTILSSEE
 LPQIFTSLSIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGTAGRLPTPSG
 TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTCGGGCGGCCTCGGAGCGCGGC
 GAGCCAGACGCTGACCACGTTCTCTCTCGGTCTCTCCGCTCCAGCTCCGCGCTGCCCG
 GCAGCCGGGAGCC**ATG**CGACCCAGGGCCCCGCCCTCCCCGAGCGGCTCCGCGGCTCC
 TGCTGCTCTGTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTATTCCGGGTACACCTG
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGCTCGAGGAAAAGCTTTGAG
 GAGTCTGGACACCCAAC TACAAGCAGTGTT CATGGAGTTCATTGAATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTG TACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT
 TCAGTGGCTCACTTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC
 AATGGAGCTGAATGTT CAGGACCTCTTCCATTGAAGCTATAATTTATTTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAAA
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAACTACCAAAA**TA**
AATGCTTTAATTTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCATTAAAT
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA
 CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT
 GGTTCATATTTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCCTCTCAACCTA
 TAATTGGAATATGTGTTGGTCTTTGTTTTTCTCTTAGTATAGCATTTTTTAAAAAATA
 TAAAGCTACCAATCTTTGTACAATTTGTAATGTTAAGAATTTTTTTTATATCTGTTAAAT
 AAAAATTATTTCCAACA

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FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393

><subunit 1 of 1, 243 aa, 1 stop

><MW: 26266, pI: 8.43, NX(S/T): 1

MRPQGPAASPQRLRGLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217